

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:05:20 ; Search time 11.62 Seconds

(without alignments)  
380.289 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLRFYVFLKGLFTAQ.....PPSFAYGKGYDKPLLANGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199.5	28.6	140	1	FKB2_MOUSE
2	195.5	28.0	217	1	FK21_NEUCR
3	188.5	27.0	141	1	FKB2_HUMAN
4	182	26.1	581	1	FKB2_MOUSE
5	176.5	25.3	135	1	FKB2_YEAST
6	144	20.6	114	1	FKBP_YEAST
7	142.5	20.4	223	1	FKB3_RABIT
8	142.5	20.4	224	1	FKB3_BOVIN
9	142.5	20.4	392	1	FKB4_YEAST
10	142	20.3	120	1	FKBP_NEUCR
11	139.5	20.0	224	1	FKB3_HUMAN
12	139.5	20.0	224	1	FKB3_MOUSE
13	138.5	19.8	124	1	FKBP_CANAL
14	135.5	19.4	411	1	FKB1_DROME
15	135.5	19.4	411	1	FKB3_YEAST
16	134	19.2	559	1	FKB7_WHEAT
17	133.5	19.1	109	1	FKBP_NEIMA
18	133.5	19.1	109	1	FKBP_NEIMB
19	133	19.1	107	1	FKB1_BOVIN
20	132.5	19.0	457	1	FKB5_HUMAN
21	131	18.8	457	1	FKB4_RABIT
22	130.5	18.7	107	1	FKB1_RAT
23	130	18.6	107	1	FKB1_HUMAN
24	129.5	18.6	412	1	FKB4_SPOPR
25	128.5	18.4	112	1	FKBP_SCHRO
26	128.5	18.4	357	1	FKB4_DROME
27	124.5	17.8	456	1	FKB5_MOUSE
28	124	17.8	107	1	FKB1_MOUSE
29	124	17.8	124	1	FKBP_STRCH
30	124	17.6	458	1	FKB4_MOUSE
31	122.5	17.5	231	1	FKB2_METJA
32	122	17.5	459	1	FKB4_HUMAN
33	119	17.0	107	1	FKB1_XENLA

## ALIGNMENTS

34	119	17.0	107	1	FKB2_MOUSE	P97534 rattus norv
35	116	16.6	107	1	FKB2_MOUSE	Q16645 homo sapien
36	111	15.9	361	1	FKB4_SCHPO	O74191 schizosacch
37	104.5	15.0	157	1	FKB1_METJA	O57726 methanococc
38	103	14.8	362	1	YAV6_SCHPO	Q10175 schizosacch
39	100.5	14.4	268	1	FKB4_AERHY	O08437 aeromonas h
40	97.5	14.0	230	1	MIP_COXBU	P51752 coxiella bu
41	95.5	13.7	154	1	FKBP_METTL	O52980 methanococc
42	89.5	12.8	270	1	FKB4_ECOLI	P45523 escherichia
43	88.5	12.7	243	1	MIP_LEBMT	P31106 legionella
44	88	12.6	205	1	FKB2_ECOLI	P39311 escherichia
45	87.5	12.5	241	1	FKB2_HAEIN	P44760 haemophilus

RESULT 1  
ID FKB2\_MOUSE STANDARD; PRT; 140 AA.

AC P45878;  
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE FK506-BINDING PROTEIN PRECURSOR (FKBP-13) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (EC 5.2.1.8).

GN FKBP2 OR FKBP13.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SVJ; TISSUE=Liver;

RX MEDLINE=94085790; PubMed=7505249;

RA Burakoff S.J., Dillella A.G.;

RT "Structural organization of the genes encoding human and murine FK506-binding protein (FKBP) 13 and comparison to FKBP1."

RL Gene 134:271-275(1993).

CC - FUNCTION: PIPIASES ACCELERATE THE FOLDING OF PROTEINS.

CC - CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

CC - PEPTIDE BONDS IN OLIGOPEPTIDES.

CC - SUBCELLULAR LOCATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.

CC - ASSOCIATED (PROBABLE).

CC - SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY.

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CC EMBL; M77831; AAA37631.1; -

CC HSSP; P20081; IYAT.

CC MGD; MGI:95542; Fkbp2.

CC InterPro; IPR001179; -

DR Pfam; PF00254; FKBP; 1.

DR PROSITE; PS00453; FKBP\_PIPIASE\_1; 1.

DR PROSITE; PS00454; FKBP\_PIPIASE\_2; 1.

DR PROSITE; PS50059; FKBP\_PIPIASE\_3; 1.

KW Isomerase; Rotamase; Signal; Endoplasmic reticulum.

FT SIGNAL 1

FT CHAIN 23

FT SITE 137

FT SITE 140

SO SEQUENCE 140 AA; 15344 MM; P4E7FCC7766A0416 CRC64;

Query Match 28.6%; Score 199.5; DB 1; Length 140;

Best local Similarity 46.8%; Pred. No. 1,9e-13;

	Matches	44;	Conservative	15;	Mismatches	32;	Indels	3;	Gaps	2;
OY	26	ESTEEVKIEVLHRENCSTKSKGDLINAHYDGLADKGSEFYCSRQNECHPKWFLGV	85							
Db	24	EGRKRRLIGVAKRVDHPIDIKSRKGDVLMHHMTGL-DGEFDSLSLPNQ--PVEFSLGT	80							
OY	86	GOVIKGLDIAMTDMCPGKKRVVIPSPFAVGKEG	119							
Db	81	GOVIKMGDOGLGMCEGKKRTLVIPSELGIQERG	114							
RESULT	2									
ID	FK21_NEUCR	STANDARD:	PRT:	217 AA.						
AC	FK21_NEUCR	060046:								
DT	15-DEC-1998	(Rel. 37, Created)								
DT	15-DEC-1998	(Rel. 37, Last sequence update)								
DE	15-JUL-1999	(Rel. 38, Last annotation update)								
Dt	FK506-BINDING PROTEIN PRECURSOR (FKBP-21) (PEPTIDYL-PROLYL CIS-									
DE	TRANS ISOMERASE) (PIPAE) (EC 5.2.1.8).									
GN	FKBP-21.									
OS	Neurospora crassa.									
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;									
OX	Sordariales; Sordariaceae; Neurospora.									
RN	NCB1_Taxid=5141;									
RP	[1]									
RC	SEQUENCE FROM N.A.									
RA	Strain-74-OR23-1A;									
CC	Solscheid B., Tropeschug M.; to the EMBL/GenBank/DDAJ databases.									
CL	Submitted (May-1998) to the EMBL database as accession U00002.									
CC	- FUNCTION: PIPASIS ACCELERATE THE FOLDING OF PROTEINS.									
CC	- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC									
CC	- PEPTIDE BONDS IN OLIGOPEPTIDES.									
CC	- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (POTENTIAL).									
CC	- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPASE FAMILY.									
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CC	use by non-profit institutions as long as its content is in no way									
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/									
CC	or send an email to licensese@sib.slb.ch).									
DR	EMBL, AJ006297; CA006962.1; -									
DR	InterPro: IPR000886; -									
DR	InterPro: IPR001179; -									
DR	pIam: PF00254; FKBP; 1.									
DR	PROSITE: PS00453; FKBP_PIPASE_1; FALSE NEG.									
DR	PROSITE: PS00454; FKBP_PIPASE_2; 1.									
DR	PROSITE: PS50059; FKBP_PIPASE_3; 1.									
DR	PROSITE: PS00014; ER_TARGET; 1.									
FT	Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.									
FT	SIGNAL	1	20	POTENTIAL.						
FT	CHAIN	21	217	FK506-BINDING PROTEIN.						
FT	Site	214	217	PREVENT SECRETION FROM ER (POTENTIAL).						
SEQ	SEQUENCE	217 AA;	22915 MW;	72313067521BCDAF CRC64;						
Query Match		28.0%;	Score 195.5;	DB 1;	Length 217;					
Best Local Similarity		45.1%;	Pred. No. 7.8e-13;							
Matches	41;	Conservative	15;	Mismatches	32;	Indels	3;	Gaps	2;	
OY	27	STEFEVKTIVLHRENCSKTSKGDLLNAHYDGLADSGKSFRQNCGHPKFWEVLGYG	86							
Db	20	AABELGSDVT-VVECDKTRKCKDKLNVAHRGLGSNGQQFDLAS-YDGTFPSFSLGGG	76							
OY	87	OVITKGLDIAMTDMCPGKKRVVIPSPFAVGK	117							
Db	77	OVITKMGDELAVDMCIGEKRTLTVPPSYGQG	107							
RESULT	3									

	ID	FKB2-HUMAN	STANDARD;	PRT:	141 AA.
	AC	FKB2.HUMAN P26885;			
Dt	01-AUG-1992	(Rel. 23, Created)			
Dt	01-AUG-1992	(Rel. 23, Last sequence update)			
Dt	15-JUL-1999	(Rel. 38, last annotation update)			
De	FKS06-BINDING PROTEIN PRECURSOR (FKBP-13) (PEPTIDYL-L-PROLYL CIS-TRANS ISOMERASE) (PIPASe) (EC 5.2.1.8).				
DE	FKBP2 OR FKBP13.				
RN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Colon carcinoma;				
RX	MEDLINE=G9131747; PubMed=1713687;				
RA	Jin Y.-J., Albers M.W., Lane W.S., Blerer B.E., Schreiber S.L., Butkoff S.J. ;				
RT	"Molecular cloning of a membrane-associated human FKS06- and rapamycin-binding protein, FKBP-13." ;				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681(1991). [2]				
RX	SEQUENCE FROM N.A.				
RA	MEDLINE=g9112052; Pubmed=1281998;				
RT	Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.;				
RL	"Chromosomal band assignments of the genes encoding human FKBP12 and FKBP13."				
CC	Biochim. Biophys. Res. Commun. 189:819-823(1992).				
CC	-I- FUNCTION: PIPASes ACCELERATE THE FOLDING OF PROTEINS.				
CC	-I- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.				
CC	-I- ENZYME REGULATION: INHIBITED BY BOTH FKS06 AND RAPAMYCIN.				
CC	-I- SUBCELLULAR LOCATION: ENDOPLASTMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLE).				
CC	-I- TISSUE SPECIFICITY: T-CELLS AND THYMUS.				
CC	-I- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL; M65128; AAA58473.1; .				
DR	EMBL; M75099; AAA36563.1; .				
DR	PIR; JC1365; JC1365.				
DR	HSSP; P20071; LFRT.				
DR	MIM; 186946; .				
DR	InterPro; IPR001179; .				
DR	Pfam; PF00254; FKBP_1.				
DR	PROSITE; PS00453; FKBP_PPIASE_1; 1.				
DR	PROSITE; PS00454; FKBP_PPIASE_2; 1.				
DR	PROSITE; PSS0059; FKBP_PPIASE_3; 1.				
KW	Isomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism.				
FT	SIGNAL	1..21			
FT	CHAIN	22..141			
FT	SITE	138..141			
FT	VARIANT	21..21			
FT					
FT	VARIANT	24..24			
FT					
FT	VARIANT	96..96			
FT					
SO	SEQUENCE	141 AA; 15654 MW; 9FA75ICA7D82D064 CRC64;	/FTId-VAR_006412. Y->C. /FTId-VAR_006411. T->A. PREVENT SECRETION FROM ER (POTENTIAL).		
	Query Match	27.0%; Score 188.5; DB 1; Length 141;			
	Best Local Similarity	45.7%; Pred. No. 2,5e-12;			
	Matches	43; Conservative 15; Mismatches 33; Indels 3; Gaps 2			

QY 26 ESTEYKLEVLHRRPENCSTKSKGDLNNAHYDGLAKDGSFYSRTQNECHPKWFLVGV 85  
 DB 25 BGKRLQIGVKKRVHCHPIKSKRGDVLHMYTKGL-EDGTEFDSLSLPGNQ--PPIVFSIGT 81  
 QY 86 GOVIGKGLIAMTDMCGEKKRVVIPPSPAYGKEG 119  
 DB 82 GOVIGKMDGDLGMYEGEKKRLVTPSELGVEG 115

RESULT 4  
 ID FBKX\_MOUSE STANDARD; PRT; 581 AA.  
 AC 061576;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE 65 KDA FK506-BINDING PROTEIN PRECURSOR (EC 5.2.1.8) (FKBP65) (FKBPRP)  
 DE (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (NOTAMASE)  
 DE (IMMUNOPHILIN FKBP65)  
 GN FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBP-RP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-JB6; TISSUE-Epidermis;  
 RA MEDLINE=94117013; PubMed=7507077;  
 RA Simek S.L., Kozak C.A., Winterstein D., Hegamyer G., Colburn N.H.;  
 RT "Sequence and localization of a novel FK506-binding protein to mouse  
 RT chromosome 11";  
 RL Genomics 18:407-409(1993).  
 [2]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RA MEDLINE=96094328; PubMed=7493967;  
 RA Coss M.C., Winterstein D., Sowder R.C., Simek S.L.;  
 RT "Molecular cloning, DNA sequence analysis, and biochemical  
 RT characterization of a novel 65-kDa FK506-binding protein (FKBP65).";  
 RL J. Biol. Chem. 270:29336-29341(1995).  
 CC -1- FUNCTION: PIPASES ACCELERATE THE FOLDING OF PROTEINS DURING  
 CC PROTEIN SYNTHESIS.  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT  
 CC BY CYCLOSPORINE A.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASTIC RETICULUM (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, SPLEEN, HEART, BRAIN  
 CC AND TESTIS.  
 CC -1- PTM: GLYCOSYLATED AND PHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PIPIASE FAMILY. CONTAINS 4  
 CC FKBP-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
 CC  
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 CC  
 CC -----  
 CC EMBL: L07063; AAC37678.1; -  
 CC MGD: MGI:104769; FKBP6.  
 CC InterPro: IPR000886; -  
 CC InterPro: IPR001179; -  
 CC InterPro: IPR002048; -  
 CC Pfam: PF00254; FKBP; 4.  
 CC Pfam: PF00036; efhand; 2.  
 CC PROSITE: PS00453; FKBP\_PIPIASE\_1; FALSE\_NEG.  
 CC PROSITE: PS00454; FKBP\_PIPIASE\_2; 1.  
 CC PROSITE: PS00059; FKBP\_PIPIASE\_3; 4.  
 CC PROSITE: PS00014; ER\_TARGET; 1.  
 CC PROSITE: PS00018; EF\_HAND; 1.

KM Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT SIGNAL 1 33  
 FT CHAIN 34 581  
 FT DOMAIN 54 146  
 FT DOMAIN 179 258  
 FT DOMAIN 291 370  
 FT DOMAIN 389 482  
 FT CA\_BIND 509 520  
 FT CA\_BIND 554 565  
 FT CARBOHYD 69 69  
 FT CARBOHYD 181 181  
 FT CARBOHYD 293 293  
 FT CARBOHYD 309 309  
 FT CARBOHYD 351 351  
 FT CARBOHYD 392 392  
 FT CARBOHYD 406 406  
 FT SITE 578 581  
 SQ SEQUENCE 581 AA; 64669 MW; 1B51B3032089E555 CRC64;

Query Match 26.1%; Score 182; DB 1; Length 581;  
 Best Local Similarity 37.9%; Pred. No. 5, 5e-11;  
 Matches 39; Conservative 24; Mismatches 30; Indels 10; Gaps 4;

QY 28 TEEVKLEVLHRR-PENCSTKSKGDLNNAHYDGLAKDGSFYSRTQNECHPKWFLVGV 86  
 DB 376 SDVEVKITLSRPENCNEKSKIGDFRIRYHNCSL-DGRLRSSHDYEA--POEITLGAN 432

QY 87 QVIGKGLIAMTDMCGEKKRVVIPPSPAYGKEGYDKPLAKGI 129  
 DB 433 KVIEGLDRGLQGCWCGERRQLIVPPLAHGENG-----ARGV 469

RESULT 5  
 ID FBK2\_YEAST STANDARD; PRT; 135 AA.  
 AC P32472;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FK506-BINDING PROTEIN PRECURSOR (FKBP-13) (FKBP-15) (PEPTIDYL-PROLYL  
 DE CIS-TRANS ISOMERASE) (PIPIASE) (EC 5.2.1.8).  
 GN PPR2 OR FKBP2 OR YDR519W OR YDR719.24.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93070605; PubMed=1279908;  
 RA Parlatadis J.A., Fleming M.A., Harding M.W., Berlin V.;  
 RT "Saccharomyces cerevisiae contains a homolog of human FKBP-13, a  
 RT membrane-associated FK506/rapamycin binding protein.";  
 RL Yeast 8:673-680(1992).  
 [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-54.  
 RA MEDLINE=92366483; PubMed=1380159;  
 RA Nielsen J.B., Foor F., Stiekerka J.J., Hsu M.J., Ramadan N.,  
 RA Motlin N., Shafiee A., Dahl A., Brizuela L., Chretien G.,  
 RA Bostian K.A., Parent S.A.;  
 RT "Yeast FKBP-13 is a membrane-associated FK506-binding protein encoded  
 RT by the nonessential gene FBK2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7471-7475(1992).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,  
 RA Benito A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,  
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,  
 RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,  
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,  
 RA Wiant A., Yelton M., Botstein D., Davis R.W.;  
 RL submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.







Query Match 20.3%; Score 142; DB 1; Length 120;  
 Best Local Similarity 41.9%; Pred. No. 1.1e-07;  
 Matches 36; Conservative 12; Mismatches 34; Indels 4; Gaps 3;

QY 31 VKIEVLHRENGSKSKGDLNANHYDGLAADSKFCSKRNQNGHKKWFLVGVGYIK 90  
 DB 9 LOIEVQOEQGTRET-RKDDNDVHHKGLV-SGKKFPAS--YDRGEPLNFTVGOGVYIK 64  
 QY 91 GUDIAMTDMCPGKKRRVVPSPFAYG 116  
 DB 65 GWDEGLGKMKIGEKRRKRLTAPHLAYG 90

RESULT 11  
 FRB3\_HUMAN STANDARD; PRT; 224 AA.  
 ID FRB3\_HUMAN Q14317;  
 AC Q00688; Q14317;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE RAPAMYCIN-SELECTIVE 25 KDA IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL  
 DE CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PIPIASE) (ROTAMASE).  
 GN FKBP3 OR FKBP25.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92287110; PubMed=1376117;  
 RA Wiederech G., Martin M., Sigal N., Slekierka J.J.;  
 RT "Isolation of a human cDNA encoding a 25 kDa FK-506 and rapamycin  
 RT binding protein.";  
 RL Biochem. Biophys. Res. Commun. 185:298-303(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92246959; PubMed=1374240;  
 RA Hung D.T., Schreiber S.L.;  
 RT "CDNA cloning of a human 25 kDa FK506 and rapamycin binding protein.";  
 RL Biochem. Biophys. Res. Commun. 184:733-738(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Thymus;  
 RA MEDLINE=92283784; PubMed=1375932;  
 RA Jin Y.-J., Burakoff S.J., Biserer B.E.;  
 RT "Molecular cloning of a 25-kDa high affinity rapamycin binding  
 RT protein, FKBP25.";  
 RL J. Biol. Chem. 267:10942-10945(1992).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 109-224.  
 RA Liang J., Hung D.T., Schreiber S.L., Clardy J.;  
 RT Submitted (SEP-1995) to the PDB data bank.  
 CC -1- FUNCTION: FK506- AND RAPAMYCIN-BINDING PROTEINS (FKBPs) CONSTITUTE  
 CC A FAMILY OF RECEPTORS FOR THE TWO IMMUNOSUPPRESSANTS WHICH INHIBIT  
 CC T CELL PROLIFERATION BY ARRESTING TWO DISTINCT CYTOPLASMIC SIGNAL  
 CC TRANSMISSION PATHWAYS.  
 CC -1- FUNCTION: PIPASES ACCELERATE THE FOLDING OF PROTEINS.  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- ENZYME REGULATION: INHIBITED PREFERENTIALLY BY RAPAMYCIN OVER  
 CC FK506.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
 CC FRAMESHIFT IN POSITION 197.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL; M96256; AAA58477.1; -;  
 DR EMBL; M90309; AAA58475.1; -;  
 DR EMBL; M90820; AAA58474.1; ALT\_FRAME.  
 DR PIR; J01522; J01522.  
 DR PDB; 1PBK; 14-OCT-96.  
 DR MIM; 186947; -;  
 DR InterPro; IPR001179; -;  
 DR Pfam; PF00254; FKBP\_1;  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1;  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2;  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3;  
 KW Isomerase; Rotamase; Nuclear protein; 3D-structure.  
 FT DOMAIN 128 224  
 FT CONFLICT 181 181  
 FT SEQUENCE 224 AA; 25177 MW; C144C5AABVEA9522 CRC64;

Query Match 20.0%; Score 139.5; DB 1; Length 224;  
 Best Local Similarity 30.4%; Pred. No. 3.9e-07;  
 Matches 42; Conservative 23; Mismatches 38; Indels 35; Gaps 5;

QY 16 LFTAKOKKEBSETEVKIEVLH-----RPENC-----SKTS-- 46  
 DB 66 LFTFKRKGTESISKVSQYKVNKLNEDEKPKETSEETLDEGPPKYTKSVLKKGDKTNP 125

QY 47 KKGDLNANHYDGLAADSKF-----YCSRTQNEGHPKRWFLVGVGYIKGDIAMTDKCP 101  
 DB 126 KKGDVHCHWTGTL-QGTYFDNINOTSAKKRNARPLSKVGKVGIVGWDEALLTMSK 184

QY 102 GKKRNVVPPSPFAYGKGG 119  
 DB 185 GEARLEIEPEMAYGKKG 202

RESULT 12  
 FRB3\_MOUSE STANDARD; PRT; 224 AA.  
 ID FRB3\_MOUSE Q62446; Q9WTJ7;  
 AC Q62446; Q9WTJ7;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE RAPAMYCIN-SELECTIVE 25 KDA IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL  
 DE CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PIPIASE) (ROTAMASE).  
 GN FKBP3 OR FKBP25.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=telencephalon;  
 RA Mas C., Bourgeois F., Simonneau M.;  
 RT "Isolation and mapping assignment of cDNAs differentially expressed in  
 RT embryonic telencephalon.";  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ahn J., Kratowicz S., Murphy M., Wang A., Levine A.J., George D.L.;  
 RT "Down-regulation of the Statmin/Op18 and FKBP25 genes following p53  
 RT expression.";  
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 168-224 FROM N.A.  
 RA MEDLINE=97115879; PubMed=8956998;  
 RA Murphy M., Hinman A., Levine A.J.;  
 RT "Wild type p53 negatively regulates a microtubule associated  
 RT protein.";  
 RL Genes Dev. 10:2971-2980(1996).  
 CC -1- FUNCTION: FK506- AND RAPAMYCIN-BINDING PROTEINS (FKBPs) CONSTITUTE  
 CC A FAMILY OF RECEPTORS FOR THE TWO IMMUNOSUPPRESSANTS WHICH INHIBIT  
 CC T CELL PROLIFERATION BY ARRESTING TWO DISTINCT CYTOPLASMIC SIGNAL  
 CC TRANSMISSION PATHWAYS (BY SIMILARITY).

```
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506 AND ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PRIPASE FAMILY.
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-----
CC EMBL; M84759; AAA34367.1; -.
CC PIR; JN0320; JN0320.
CC HSSP; P20081; LYAT.
CC InterPro; IPR001179; .
CC Pfam; PF00254; FKBP; 1.
CC PROSITE; PS00453; FKBP_PRIPASE_1; 1.
CC PROSITE; PS00454; FKBP_PRIPASE_2; 1.
CC PROSITE; PSS0059; FKBP_PRIPASE_3; 1.
CC Isomerase; Notmanse.
KW SEQUENCE 124 AA; 13227 MW; CC7DA60FFBEF72242 CRC64;
SQ
Query Match 19.8%; Score 138.5; DB 1; Length 124;
Best Local Similarity 36.5%; Pred. No. 2.6e-07;
Matches 38; Conservative 16; Mismatches 35; Indels 15; Gaps 4;
OY 27 STEEVKIEVLRHRENSCKTSKKGLLNHYGYIAKGDSKYTCRTONEGHPKFVLGVG 86
| | : : : : : | : | : | : | : | : | : | : | : | : | : ||||
Db 2 SELQPIETIVEGDN-TTFAPRGDVTIITHYGDKLT-NKEPEDSR--KRGPFTCTIVGG 57
OY 87 QYIKGLDIAMTD-----MCGEKKRVVPPEPFAYGREG 119
||||| |:|::| : : : : : : : : : : : : : : : : : : :
Db 58 QYIKGMIDISLTNNNGSGCANLPKISKGTALITTPNALVPGR 101
RESULT 14
FKBL_DROME STANDARD; PTR; 108 AA.
AC P48375;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DL 01-JUL-1999 (Rel. 38, Last annotation update)
DE 12 KDA FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PRIASE) (EC 5.2.1.8) (MACROLIDE BINDING PROTEIN).
GN FK506-BP2 OR FKBP12.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CANTON-S; Tissue=Head;
RA Submitted (Apr-1995) to the EMBL/GenBank/DDBJ databases.
RL [2]
RN RP SEQUENCE FROM N.A.
RA Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,
RA Lechler R.J., Martin J., Mangano A.T., Donahoe P.K.;
RL Submitted (Mar-1996) to the EMBL/Genbank/DDBJ databases.
CC -1- FUNCTION: PRIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PRIPASE FAMILY.
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DR EMBL: 249079; CAA8904.1; -  
 DR EMBL: U41441; AAB91178.1; -  
 DR HSSP: P20071; IPRK  
 DR FLYBase: FBgn0013954; FK506-bp2.  
 DR InterPro: IPR001179; -  
 DR Pfam: PF00254; FKBP.1.  
 DR PROSITE: PS00453; FKBP\_PPIASE.1; 1.  
 DR PROSITE: PS00454; FKBP\_PPIASE.2; 1.  
 DR PROSITE: PS00509; FKBP\_PPIASE.3; 1.  
 KW isomerase; Rotamase.  
 SQ SEQUENCE 108 AA; 11597 MW; 48BCE993AC8D350A CRC64;

Query Match 19.4%; Score 135.5; DB 1; Length 108;  
 Best Local Similarity 36.6%; Pred. No. 4,4e-07;  
 Matches 30; Conservative 15; Mismatches 34; Indels 3; Gaps 2;

QY 39 PENCSTKSKKDLLNAHYDGLAKDGSFKYSTRONEGHPKFWYLGVGQVTKGLDIAMTD 98  
 D 10 PGDSTYKPKNGOKVYHTGTL-DDGTFPDSRRNK--PKFTTGKGEVIRGWDGVAQ 66  
 QY 99 MCPGEKRVVLPSPFAYGKEV 120  
 D 67 LSVGOSAKLICSPDYAVGSRGH 88

RESULT 15  
 FKBP\_YEAST STANDARD; PRT; 411 AA.  
 AC P38911;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)  
 DE (PIRASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE  
 DE ISOMERASE) (FKBP-70).  
 GN FPR3 OR NP146 OR YML074C.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YNM 214;  
 RX MEDLINE=95050937; PubMed=7525596;  
 RA Benton B.M., Zang J.-H., Thorner J.;  
 RT "A novel FK506- and rapamycin-binding protein (FPR3 gene product) in  
 RT the yeast *Saccharomyces cerevisiae* is a proline rotamase localized to  
 RT the nucleolus.";  
 RL J. Cell Biol. 127:623-639(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=94327703; PubMed=8051210;  
 RA Shan X., Xue Z., Melese T.;  
 RT "Yeast NP146 encodes a novel prolyl cis-trans isomerase that is  
 RT located in the nucleolus.";  
 RL J. Cell Biol. 126:853-862(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95010686; PubMed=7925954;  
 RA Manning-Krieg U.C., Henriquez R., Cammas F., Grafi P.,  
 RA Gaveriaux S., Moya N.R.;  
 RT "Purification of FKBP-70, a novel immunophilin from *Saccharomyces*  
 RT *cerevisiae*, and cloning of its structural gene, FPR3.";  
 RL FEBS Lett. 352:98-103(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;

RA Brown D., Bowman S., Barrell B.G., Rajandream M.A.;  
 RL Submitted (OCT-1994) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP PHOSPHORYLATION OF TYR-184 AND SER-186.  
 RX MEDLINE=97294697; PubMed=9148902;  
 RA Wilson L.K., Dhillon N., Thorner J., Martin G.S.;  
 RT "Casein kinase II catalyzes tyrosine phosphorylation of the yeast  
 RT nucleolar immunophilin Fpr3.";  
 RL J. Biol. Chem. 272:12961-12967(1997).  
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FK506- AND  
 CC RAPAMYCIN-BINDING PROTEIN. SPECIFICALLY BINDS NUCLEAR LOCALIZATION  
 CC SEQUENCES. MAY BE INVOLVED IN THE ASSEMBLY OR FOLDING OF RIBOSOMAL  
 CC PROTEINS.  
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC  
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.  
 CC -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.  
 CC -1- PTM: PHOSPHORYLATED AT TYROSINE AND DEPHOSPHORYLATED BY THE  
 CC PHOSPHOTYROSINE-SPECIFIC PHOSPHOPROTEIN PHOSPHATASE PTP1.  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.

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DR EMBL: L34569; AAB04165.1; -  
 DR EMBL: X79379; CAA55924.1; -  
 DR EMBL: S73876; AAB31995.1; -  
 DR EMBL: Z46373; CAA86504.1; -  
 DR PIR: S47927; S47927.  
 DR PIR: A53544; A53544.  
 DR HSSP: P20081; IYAT.  
 DR SGD: S0004539; NP146.  
 DR InterPro: IPR001179; -  
 DR Pfam: PF00254; FKBP.1.  
 DR PROSITE: PS00453; FKBP\_PPIASE.1; 1.  
 DR PROSITE: PS00454; FKBP\_PPIASE.2; 1.  
 DR PROSITE: PS00509; FKBP\_PPIASE.3; 1.  
 KW isomerase; Rotamase; Nuclear protein; phosphorylation.  
 FT DOMAIN 60 87 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 88 99 LYS-RICH (HIGHLY BASIC).  
 FT DOMAIN 101 119 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 173 248 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 250 298 LYS-RICH (HIGHLY BASIC).  
 FT DOMAIN 324 411 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 184 184 PPIASE, FKBP-TYPE.  
 FT MOD\_RES 186 186 PHOSPHORYLATION (BY CK2).  
 FT CONFLICT 122 122 PHOSPHORYLATION (BY CK2).  
 FT CONFLICT 240 240 L->P (IN REF. 1).  
 FT CONFLICT 240 240 E->EER (IN REF. 1).  
 FT CONFLICT 335 335 L->F (IN REF. 1).  
 SQ SEQUENCE 411 AA; 46555 MW; A01D24DE0078FE11 CRC64;

Query Match 19.4%; Score 135.5; DB 1; Length 411;  
 Best Local Similarity 34.3%; Pred. No. 2e-06;  
 Matches 37; Conservative 16; Mismatches 44; Indels 11; Gaps 3;

QY 18 TAQRKKEESTEEVKEIVLH-----RPENCSTKSKKDLLNAHYDGLAKDGSFKYCS 70  
 D 286 TPKRSKTRKEDKHKPKSKVLEGGIVIEDTIDGDPKAKGAVGMRITGKL-KNKRVF--- 341  
 QY 71 RTQNGHGRKWFVLGVGYIKGLDIAMTDMCGEKKRVVLPSPFAYGKE 118  
 D 342 DKNISGKPFKRLRGVYIKGWDIGVAGMSVGGERRRIIPAPYAVGRO 389

Fri Aug 31 12:10:26 2001

us-09-622-522-1.rsp

Page 10

Job time: 98 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:04 ; Search time 21.29 Seconds

(without alignments)  
367.332 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLFRFVFFYLMGLFTAAQ.....PPSFAYKRGYDKPLAKGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

A\_Geneseq\_0601:\*

- 1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseqp/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseqp/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseqp/AA1985.DAT.\*
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- 19: /SID88/gcgdata/geneseq/geneseqp/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseqp/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	698	100.0	129	20	Transmembrane doma
2	653	93.6	219	20	Secreted protein e
3	653	93.6	222	21	Human PRO1304 prot
4	653	93.6	222	21	Human PRO1304 (UNQ
5	653	93.6	222	22	Protein of the inv
6	653	93.6	222	22	Human PRO1304 prot
7	648	92.8	222	21	Amino acid sequenc
8	344	49.3	68	21	Human 5' EST relat
9	275	39.4	57	20	Secreted protein e
10	271.5	38.9	211	20	Human PRO381 prote
11	271.5	38.9	211	20	Polypeptide fragme

12	271.5	38.9	211	21	AAAB44262	Human PRO381 (UNQ3
13	271.5	38.9	211	21	AAAB24021	Human PRO381 prote
14	271.5	38.9	211	21	AAAB33463	Human PRO381 prote
15	271.5	38.9	211	21	AAAY94975	Human secreted pro
16	271.5	38.9	211	22	AAAB50909	Human PRO381 prote
17	271.5	38.9	211	22	AAAB50952	Human PRO381 prote
18	271	38.8	186	20	AAAY01459	Polypeptide fragme
19	269.5	38.6	118	20	AAAY27131	Human embryonal li
20	269.5	38.6	131	22	AAAB67049	Human immune respo
21	264.5	37.9	212	20	AAAY01401	Secreted protein e
22	199.5	28.6	137	22	AAAB87656	Bovine mammary tis
23	199.5	28.6	141	17	AAAR93551	Human FKBP-13 immu
24	197.5	28.3	99	13	AAAR28979	Bovine FKBP. Bos
25	197	28.2	143	13	AAAB54356	Human secreted pro
26	190.5	27.3	434	21	AAAB54356	Human secreted pro
27	190	27.2	366	21	AAAB57114	Human pancreatic c
28	190	27.2	582	21	AAAB12128	Human prostate can
29	190	27.2	582	21	AAAY52294	Hydrophobic domain
30	189	27.1	441	20	AAAY23885	Amino acid sequenc
31	187.5	26.9	388	20	AAAY23887	Amino acid sequenc
32	187.5	26.9	541	20	AAAY23886	Amino acid sequenc
33	187.5	26.9	570	22	AAAB88320	Amino acid sequenc
34	187	26.8	316	20	AAAY23884	Human membrane or
35	186.5	26.7	159	21	AAAG10995	Amino acid sequenc
36	186.5	26.7	163	21	AAAG10994	Arabidopsis thalia
37	178.5	25.6	146	21	AAAG39838	Arabidopsis thalia
38	178.5	25.6	152	21	AAAG39837	Arabidopsis thalia
39	178.5	25.6	153	21	AAAG39836	Arabidopsis thalia
40	176.5	25.3	146	21	AAAG05732	Arabidopsis thalia
41	176.5	25.3	152	21	AAAG05731	Arabidopsis thalia
42	176.5	25.3	153	21	AAAG05730	Arabidopsis thalia
43	163.5	23.4	201	21	AAAB42852	Human ORFX ORF2616
44	163.5	23.4	201	21	AAAB24060	Human PRO535 prote
45	163.5	23.4	201	21	AAAB23604	Human secreted pro

#### ALIGNMENTS

RESULT 1	AAAY32922	standard; Protein: 129 AA.
XX	AAAY32922;	
AC	AAAY32922;	
XX	AAAY32922;	
DF	04-NOV-1999 (first entry)	
XX	04-NOV-1999 (first entry)	
DE	Transmembrane domain containing protein clone HPO1434.	
XX	Transmembrane domain containing protein; human; antibody production;	
KW	interaction assay; diagnosis; nutritional activity; cytokine;	
KW	cell proliferation; cell differentiation activity; immune stimulant;	
KW	immune suppressant; haematopoiesis regulator; tissue growth activity;	
KW	activin; inhibin activity; chemotaxis; chemokinesis; haemostasis;	
KW	thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor;	
KW	tumour inhibitor.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9943802-A2.	
XX		
PD	02-SEP-1999.	
XX		
PF	25-FEB-1999; 99WO-JP00875.	
XX		
PR	27-FEB-1998; 98JP-0046607.	
XX		
PA	(PROT-) PROTEGENE INC.	
PA	(SAGA) SAGAMI CHEM RES CENT.	
XX		
PI	Kato S, Kimura T, Nakamura N, Sekine S;	
XX		
DR	WPI, 1999-527617/44.	

DR N-PSDB; AA11176, AA11183.

XX New proteins and DNA useful for preventing tumours

XX Claim 1; Page 70-71; 96pp; English.

XX This sequence is a human transmembrane protein of the invention. The  
CC DNAs are useful for expressing recombinant protein for analysis,  
CC characterisation or therapeutic use, and are useful as markers for  
CC tissues in which the corresponding protein is preferentially expressed.  
CC They are also useful as molecular weight markers on Southern gels, as  
CC chromosome markers or tags (when labelled) to identify potential genetic  
CC disorders, as probes to hybridise and thus discover novel, related DNA  
CC sequences, as a source of PCR primers for genetic fingerprinting, as  
CC probes to subtract-out known sequences in the process of attachment to a  
CC gene chip or other support, including for examination of expression  
CC patterns, to raise anti-protein antibodies using DNA immunisation  
CC techniques, and as an antigen to raise anti-DNA antibodies or elicit  
CC another immune response. Where the DNA encodes a protein which binds to  
CC another protein (e.g. in a receptor-ligand interaction), the DNA can also  
CC be used in interaction trap assays to identify DNAs encoding the other  
CC protein with which binding occurs or to identify inhibitors of the  
CC binding interaction. The DNAs and proteins can have e.g. nutritional  
CC activity, cytokine and cell proliferation/differentiation activity,  
CC immune stimulating (e.g. as vaccines) or suppressing activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, cadherin/tumour invasion suppressor activity, and tumour  
CC inhibition activity.

XX Sequence 129 AA:

Query Match 100.0%; Score 698; DB 20; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.1e-75;  
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHFLRPVFPYVWGLTFAOROKKEESTEEVKIEVLRPENCSTSKSGDLNANHYGYL 60  
DB 1 mhflrpfvfywglftaqrqkkeseevklevlhrpencstsksgdlnahygy1 60  
QY 61 AKDSKFCSTQNGHPRKFWLVGVGVIGKIDAMTDMCPGKRVVIPPSPAYGKEGY 120  
DB 61 akdskfcstqngphrkfwlvigvgvixgldiamtcmcpgekrrvippsfaygkegy 120  
QY 121 DKPLAKGI 129  
DB 121 dkplakgi 129

RESULT 2

AAW88556 AAW88556 standard; Protein; 219 AA.

AAW88556;

01-MAR-1999 (first entry)

Secreted protein encoded by gene 23 clone HSGE084.

Human; secreted protein; fusion protein; gene therapy; protein therapy;  
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
developmental abnormality; foetal deficiency; blood; allergy; renal;  
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

PN W09854963-A2.

XX 10-DEC-1998.

XX 04-JUN-1998;

98WO-US11422.

18-DEC-1997; 97US-0070923.  
06-JUN-1997; 97US-0048877.  
06-JUN-1997; 97US-0048881.  
06-JUN-1997; 97US-0048884.  
06-JUN-1997; 97US-0048893.  
06-JUN-1997; 97US-0048896.  
06-JUN-1997; 97US-0048899.  
06-JUN-1997; 97US-0048915.  
06-JUN-1997; 97US-0048949.  
06-JUN-1997; 97US-0048964.  
06-JUN-1997; 97US-0048972.  
06-JUN-1997; 97US-0049020.  
05-SEP-1997; 97US-0049375.  
05-SEP-1997; 97US-0057628.  
05-SEP-1997; 97US-0057635.  
05-SEP-1997; 97US-0057644.  
05-SEP-1997; 97US-0057647.  
05-SEP-1997; 97US-0057650.  
05-SEP-1997; 97US-0057661.  
05-SEP-1997; 97US-0057667.  
05-SEP-1997; 97US-0057761.  
05-SEP-1997; 97US-0057764.  
05-SEP-1997; 97US-0057770.  
05-SEP-1997; 97US-0057775.  
05-SEP-1997; 97US-0057778.  
06-JUN-1997; 97US-0048875.  
06-JUN-1997; 97US-0048878.  
06-JUN-1997; 97US-0048882.  
06-JUN-1997; 97US-0048885.  
06-JUN-1997; 97US-0048894.  
06-JUN-1997; 97US-0048897.  
06-JUN-1997; 97US-0048900.  
06-JUN-1997; 97US-0048916.  
06-JUN-1997; 97US-0048962.  
06-JUN-1997; 97US-0048970.  
06-JUN-1997; 97US-0048974.  
06-JUN-1997; 97US-0048973.  
05-SEP-1997; 97US-0057584.  
05-SEP-1997; 97US-0057629.  
05-SEP-1997; 97US-0057642.  
05-SEP-1997; 97US-0057645.  
05-SEP-1997; 97US-0057648.  
05-SEP-1997; 97US-0057651.  
05-SEP-1997; 97US-0057662.  
05-SEP-1997; 97US-0057668.  
05-SEP-1997; 97US-0057762.  
05-SEP-1997; 97US-0057765.  
05-SEP-1997; 97US-0057771.  
05-SEP-1997; 97US-0057776.  
06-JUN-1997; 97US-0048876.  
06-JUN-1997; 97US-0048880.  
06-JUN-1997; 97US-0048883.  
06-JUN-1997; 97US-0048892.  
06-JUN-1997; 97US-0048895.  
06-JUN-1997; 97US-0048898.  
06-JUN-1997; 97US-0048901.  
06-JUN-1997; 97US-0048917.  
06-JUN-1997; 97US-0048963.  
06-JUN-1997; 97US-0048971.  
06-JUN-1997; 97US-0049019.  
06-JUN-1997; 97US-0049374.  
05-SEP-1997; 97US-0057627.  
05-SEP-1997; 97US-0057634.  
05-SEP-1997; 97US-0057643.  
05-SEP-1997; 97US-0057646.  
05-SEP-1997; 97US-0057649.  
05-SEP-1997; 97US-0057654.

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PR 05-SEP-1997; 97US-0057666.
PR 05-SEP-1997; 97US-0057760.
PR 05-SEP-1997; 97US-0057763.
PR 05-SEP-1997; 97US-0057769.
PR 05-SEP-1997; 97US-0057774.
PR 05-SEP-1997; 97US-0057777.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
PI Florence K, Greene JM, Hu J, Kyaw H, Laflaur DM;
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruden SM;
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX WPI: 1999-059865/05.
DR N-PSDB: AAV84433.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 11; Page 500-501; 772pp; English.
XX
CC The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAV88534 to AAV88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97974, 97974, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes,
CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents human secreted protein (see descriptor
CC line for gene number and clone identification).
XX
XX
SO Sequence 219 AA:

```

```

Query Match 93.6%; Score 653; DB 20; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.2e-70;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MHFLFRIVFYIWMGLTAQRORKEESTEBVKIEVLHREPCSKTSRKGDLLNAHYDGYL 60
DB 1 MHFLFRIVFYIWMGLTAQRORKEESTEBVKIEVLHREPCSKTSRKGDLLNAHYDGYL 60
QY 61 AKDGFYCSRNQNEGHPRMFWVNGOVYKGDIAITMDCCPEKRVVPPSPFAYGKEY 120
DB 61 AKDGFYCSRNQNEGHPRMFWVNGOVYKGDIAITMDCCPEKRVVPPSPFAYGKEY 120

```

```

RESULT 3
AAB24429 standard; Protein; 222 AA.
XX AAB24429;
AC AAB24429;
XX 07-NOV-2000 (first entry)
DT

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```

XX XX
DE Human PRO1304 protein sequence SEQ ID NO:205.
XX
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antithrombotic;
KW cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200032221-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28313.
XX
XX 01-DEC-1998; 98WO-US25108.
XX 16-DEC-1998; 98US-0112850.
XX 12-JAN-1999; 99US-0115554.
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0144758.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-OCT-1999; 99US-0162506.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
XX Watanabe CK, Williams PM, Wood WI;
XX WPI: 2000-412154/35.
XX N-PSDB: AAV7672.
XX
XX WPI: 2000-412154/35.
XX N-PSDB: AAV7672.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
XX diagnosing and treating disorders in mammals -
XX angiogenic disorders in mammals -
XX
XX Claim 72; Fig 84; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating disorders in mammals by
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PRO expression such as cardiovascular, endothelial or
XX angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
XX cardiac hypertrophy). For example, the nucleic acids (NAs) and vectors
XX containing them and the PRO polypeptide may be used to treat disorders
XX associated with decreased PRO expression. AAV7510 to AAV7721 and
XX AAB24388 to AAB24435 represent nucleotide and protein sequences used in
XX the exemplification of the present invention.
XX
XX
SO Sequence 222 AA:

```

```

Query Match 93.6%; Score 653; DB 21; Length 222;
Best Local Similarity 100.0%; Pred. No. 5.3e-70;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHFLFRIVFYIWMGLTAQRORKEESTEBVKIEVLHREPCSKTSRKGDLLNAHYDGYL 60

```

Db 5 mbllflfivfywglftgrqkkesteevkvlethrpenscktskkgdlInahdyj 64  
QY 61 AKDGSFYCSFRIONESHPRKFWLGVGVTKGDIANTDMCPGKKRVVLPSPFAFGKEGY 120  
Db 65 akdgsfkfycsttqeghpkwfwlgyvqvlkjdlamtcmcpkkrkvlpstfay9key 124

RESULT 4  
ID AAY9391 standard; Protein; 222 AA.  
XX AAY9391;  
AC AAY9391;  
XX 08-AUG-2000 (first entry)  
DT Human PRO1304 (UN0670) amino acid sequence SRQ ID NO:180.  
XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
XX Homo sapiens.  
XX MO200012708-A2.  
PN 09-MAR-2000.  
PD 01-SEP-1999; 99MO-U0520111.  
XX 01-SEP-1998; 98US-0098716.  
PR 01-SEP-1998; 98US-0098749.  
PR 01-SEP-1998; 98US-0098750.  
PR 02-SEP-1998; 98US-0098803.  
PR 02-SEP-1998; 98US-0098821.  
PR 02-SEP-1998; 98US-0098843.  
PR 09-SEP-1998; 98US-0099536.  
PR 09-SEP-1998; 98US-0099596.  
PR 09-SEP-1998; 98US-0099598.  
PR 09-SEP-1998; 98US-0099602.  
PR 09-SEP-1998; 98US-0099642.  
PR 10-SEP-1998; 98US-0099741.  
PR 10-SEP-1998; 98US-0099754.  
PR 10-SEP-1998; 98US-0099763.  
PR 10-SEP-1998; 98US-0099792.  
PR 10-SEP-1998; 98US-0099808.  
PR 10-SEP-1998; 98US-0099812.  
PR 10-SEP-1998; 98US-0099815.  
PR 10-SEP-1998; 98US-0099816.  
PR 15-SEP-1998; 98US-0100385.  
PR 15-SEP-1998; 98US-0100388.  
PR 15-SEP-1998; 98US-0100390.  
PR 16-SEP-1998; 98US-0100584.  
PR 16-SEP-1998; 98US-0100627.  
PR 16-SEP-1998; 98US-0100661.  
PR 16-SEP-1998; 98US-0100662.  
PR 16-SEP-1998; 98US-0100664.  
PR 17-SEP-1998; 98US-0100683.  
PR 17-SEP-1998; 98US-0100684.  
PR 17-SEP-1998; 98US-0100710.  
PR 17-SEP-1998; 98US-0100711.  
PR 17-SEP-1998; 98US-0100919.  
PR 17-SEP-1998; 98US-0100930.  
PR 18-SEP-1998; 98US-0100948.  
PR 18-SEP-1998; 98US-0100849.  
PR 18-SEP-1998; 98US-0101014.  
PR 18-SEP-1998; 98US-0101068.  
PR 18-SEP-1998; 98US-0101071.  
PR 22-SEP-1998; 98US-0101279.  
PR 23-SEP-1998; 98US-0101471.  
PR 23-SEP-1998; 98US-0101472.  
PR 23-SEP-1998; 98US-0101474.  
PR 23-SEP-1998; 98US-0101475.  
PR 23-SEP-1998; 98US-0101476.

PR 23-SEP-1998; 98US-0101477.  
PR 23-SEP-1998; 98US-0101479.  
PR 24-SEP-1998; 98US-0101738.  
PR 24-SEP-1998; 98US-0101741.  
PR 24-SEP-1998; 98US-0101743.  
PR 24-SEP-1998; 98US-0101915.  
PR 24-SEP-1998; 98US-0101916.  
PR 29-SEP-1998; 98US-0102207.  
PR 29-SEP-1998; 98US-0102240.  
PR 29-SEP-1998; 98US-0102307.  
PR 29-SEP-1998; 98US-0102330.  
PR 29-SEP-1998; 98US-0102331.  
PR 30-SEP-1998; 98US-0102484.  
PR 30-SEP-1998; 98US-0102487.  
PR 30-SEP-1998; 98US-0102570.  
PR 30-SEP-1998; 98US-0102571.  
PR 30-SEP-1998; 98US-0102571.  
PR 01-OCT-1998; 98US-0102684.  
PR 01-OCT-1998; 98US-0102687.  
PR 02-OCT-1998; 98US-0102965.  
PR 06-OCT-1998; 98US-0103258.  
PR 06-OCT-1998; 98US-0103449.  
PR 07-OCT-1998; 98US-0103314.  
PR 07-OCT-1998; 98US-0103315.  
PR 07-OCT-1998; 98US-0103328.  
PR 07-OCT-1998; 98US-0103395.  
PR 07-OCT-1998; 98US-0103396.  
PR 07-OCT-1998; 98US-0103401.  
PR 08-OCT-1998; 98US-0103633.  
PR 08-OCT-1998; 98US-0103678.  
PR 08-OCT-1998; 98US-0103679.  
PR 08-OCT-1998; 98US-0103711.  
PR 14-OCT-1998; 98US-0104257.  
PR 20-OCT-1998; 98US-0104987.  
PR 20-OCT-1998; 98US-0105000.  
PR 20-OCT-1998; 98US-0105002.  
PR 21-OCT-1998; 98US-0105104.  
PR 22-OCT-1998; 98US-0105169.  
PR 22-OCT-1998; 98US-0105266.  
PR 26-OCT-1998; 98US-0105693.  
PR 26-OCT-1998; 98US-0105694.  
PR 27-OCT-1998; 98US-0105807.  
PR 27-OCT-1998; 98US-0105881.  
PR 27-OCT-1998; 98US-0105882.  
PR 27-OCT-1998; 98US-0106062.  
PR 28-OCT-1998; 98US-0106023.  
PR 28-OCT-1998; 98US-0106029.  
PR 28-OCT-1998; 98US-0106030.  
PR 28-OCT-1998; 98US-0106032.  
PR 28-OCT-1998; 98US-0106033.  
PR 28-OCT-1998; 98US-0106178.  
PR 29-OCT-1998; 98US-0106248.  
PR 29-OCT-1998; 98US-0106384.  
PR 29-OCT-1998; 98US-0106500.  
PR 30-OCT-1998; 98US-0106464.  
PR 03-NOV-1998; 98US-0106856.  
PR 03-NOV-1998; 98US-0106902.  
PR 03-NOV-1998; 98US-0106905.  
PR 03-NOV-1998; 98US-0106919.  
PR 03-NOV-1998; 98US-0106932.  
PR 10-NOV-1998; 98US-0107783.  
PR 17-NOV-1998; 98US-0108775.  
PR 17-NOV-1998; 98US-0108779.  
PR 17-NOV-1998; 98US-0108787.  
PR 17-NOV-1998; 98US-0108788.  
PR 17-NOV-1998; 98US-0108801.  
PR 17-NOV-1998; 98US-0108802.  
PR 17-NOV-1998; 98US-0108806.  
PR 17-NOV-1998; 98US-0108807.  
PR 17-NOV-1998; 98US-0108867.  
PR 17-NOV-1998; 98US-0108925.  
PR 18-NOV-1998; 98US-0108848.  
PR 18-NOV-1998; 98US-0108849.

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PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI.
DR N-PSDB; AAA37073.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS Claim 12; Fig 104; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 222 AA:

Query Match 93.6%; Score 653; DB 21; Length 222;
Best Local Similarity 100.0%; Pred. No. 5.3e-70;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLRFPIVFEYLMGLFTAQROKKEESTEEVRIEVLHREPMCKSTSKKGLDLNHYDGYL 60
DB 5 mhlrlrfvlylwgllftaqrqkkeesteekvlevlhrpencsktskkgdlnahydy1 64
OY 61 AKDGSKFYCSRTONGHGRKWFVLGVGVYIKGLDITAMTDMCPGKRRKVIYIPSPFAYGREGY 120
DB 65 akdgskfycsrtneghgrkfwfvlgvgyikgldiamtdmcpgekrkvvipspfaygkey 124

RESULT 5
AAB66140
ID AAB66140 standard; protein; 222 AA.
XX
AC AAB66140;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #52.
XX
KW Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
PN WO200078961-A1.
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US04342.
XX
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 01-SEP-1999; 99US-0145698.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99US-0162506.
PR 02-DEC-1999; 99US-0283313.
PR 16-DEC-1999; 99US-0283313.
PR 16-DEC-1999; 99US-0283313.

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PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
DR WPI: 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy -
XX
PS Claim 1; Fig 104; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of
CC anti-sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents.
CC The nucleic acids may also be used in gene therapy.
XX
SQ Sequence 222 AA:

Query Match 93.6%; Score 653; DB 22; Length 222;
Best Local Similarity 100.0%; Pred. No. 5.3e-70;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLRFPIVFEYLMGLFTAQROKKEESTEEVRIEVLHREPMCKSTSKKGLDLNHYDGYL 60
DB 5 mhlrlrfvlylwgllftaqrqkkeesteekvlevlhrpencsktskkgdlnahydy1 64
OY 61 AKDGSKFYCSRTONGHGRKWFVLGVGVYIKGLDITAMTDMCPGKRRKVIYIPSPFAYGREGY 120
DB 65 akdgskfycsrtneghgrkfwfvlgvgyikgldiamtdmcpgekrkvvipspfaygkey 124

RESULT 6
AAB50988
ID AAB50988 standard; protein; 222 AA.
XX
AC AAB50988;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1304 protein.
XX
KW Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
KW vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW vulnerrary; antiangiinal; gene therapy; cardiovascular disease;
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW wound healing.
XX
OS Homo sapiens.
XX
PN WO200073445-A2.
PD 07-DEC-2000.
XX
PF 17-MAY-2000; 2000WO-US13705.
XX
PR 02-JUN-1999; 99US-0141037.
PR 23-JUN-1999; 99US-0144758.
PR 20-JUL-1999; 99US-0145698.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99US-0283313.
PR 30-NOV-1999; 99US-0283313.

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PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertlisen ME;  
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;  
 PI Pooni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 DR WPI: 2001-025251/03.  
 DR N-PSDB: AAC90572.

PT Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 PT disorders in a mammal -  
 PS Claim 71; Fig 20; 182pp; English.

XX The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 CC nucleic acids, polypeptides, agonists and antagonists are useful for  
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.  
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,  
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial  
 CC restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial  
 CC infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and  
 CC antagonists are also used to prevent tumour angiogenesis and for treating  
 CC periodontal diseases. They are also used to stimulate wound healing and  
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO  
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder.

XX Sequence 222 AA;

Query Match 93.6%; Score 653; DB 22; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-70;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLFRFIVFYLMGLFTAQROKKEESTEEVKIEVLHREPCSKTSKGGDLNAHYDYL 60  
 DB 5 mhflfrfivfyfllwglftagrqkkeeesteevkievhlhrencsktskkgdlnahydyll 64  
 OY 61 AKDGSKFTYCSRTQNEGHKRWYLVGVGVYIKGLDIAMTDMPGKRRKRVIPSPFAYGKEGY 120  
 DB 65 akdgskfycstqneghkwrwlvgygvlykglidiamtcmpgkrrkvipspfaygkgy 124

RESULT 7

AAV84868  
 ID AAV84868 standard; Protein: 222 AA.

AC AAV84868;

DT 08-AUG-2000 (first entry)

DE Amino acid sequence of a human FK506 binding protein (FKBP).

XX Human; FK506 binding protein; FKBP; NPAAEB04; cancer; diabetes mellitus;

XX kidney disease; autoimmune disease; metabolic disorder; vaccine;

XX gene therapy.

XX Homo sapiens.

PN WO200021992-A1.

XX 20-APR-2000.

XX 09-OCT-1998; 98WO-CN00220.

XX 09-OCT-1998; 98WO-CN00220.

XX (USH-) UNIV SHANGHAI SECOND MEDICAL.

PI Song H, Han Z, Hu R, Huang C, Ren S;

DR WPI: 2000-317939/27.

DR N-PSDB: AAA14950.

XX New polypeptide designated NPAAEB04 useful for diagnosing and treating  
 XX cancer and diabetes is thought to be FKBP5 binding protein -  
 XX Claim 1; Page 20; 32pp; English.

XX The present sequence represents a human FK506 binding protein (FKBP),  
 CC designated NPAAEB04. The protein may be used to screen for its agonists  
 CC and antagonists. Diseases or conditions arising from altered expression  
 CC or activity of NPAAEB04 may be diagnosed by detecting NPAAEB04 in a  
 CC sample from a patient or detecting a mutation in the NPAAEB04 gene in  
 CC the genome of a patient. These diseases or conditions include cancer,  
 CC diabetes mellitus, kidney disease, autoimmune diseases or metabolic  
 CC disorders. The FKBP polynucleotides and polypeptides may be administered  
 CC to patients as vaccines or as part of a gene therapy regime.  
 CC respectively, to treat these diseases or conditions.

XX Sequence 222 AA;

Query Match 92.8%; Score 648; DB 21; Length 222;  
 Best Local Similarity 99.2%; Pred. No. 2.1e-69;  
 Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MHFLFRFIVFYLMGLFTAQROKKEESTEEVKIEVLHREPCSKTSKGGDLNAHYDYL 60  
 DB 5 mhflfrfivfyfllwglftagrqkkeeesteevkievhlhrencsktskkgdlnahydyll 64

OY 61 AKDGSKFTYCSRTQNEGHKRWYLVGVGVYIKGLDIAMTDMPGKRRKRVIPSPFAYGKEGY 120  
 DB 65 akdgskfycstqneghkwrwlvgygvlykglidiamtcmpgkrrkvipspfaygkgy 124

RESULT 8

AAV65390  
 ID AAV65390 standard; Protein: 68 AA.

AC AAV65390;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:1551.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;

XX gene therapy; chromosome mapping; upstream regulatory sequence;

XX forensic; location; development; protein synthesis; stability;

XX regulation; identification.

XX Homo sapiens.

XX 21-OCT-1999.

XX 09-APR-1999; 99WO-IB00712.

XX 09-APR-1998; 98US-0057719.

XX 28-APR-1998; 98US-0069047.



PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-038446/03.  
 DR N-PSDB; AAZ43004.  
 XX  
 PT Novel secreted protein 5' expressed sequence tag sequences used in  
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures  
 XX  
 PS Claim 3; Page 817; 837pp; English.  
 XX  
 CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)  
 CC sequences, corresponding to human secreted proteins. AAY64651 to  
 CC AAY64658 represent the EST-related proteins corresponding to AAZ42265 to  
 CC AAZ43052. The 5' ESTs can be used for producing secreted human gene  
 CC products. They can be used to identify and isolate 5' untranslated  
 CC regions (UTRs) and upstream regulatory regions which control the  
 CC location, development stage, rate, and quantity of protein synthesis, as  
 CC well as stability of mRNA. The ESTs are also useful as probes for  
 CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can  
 CC also be used in forensic procedures to identify individuals, or in  
 CC diagnostic procedures to identify individuals having genetic diseases  
 CC resulting from abnormal gene expression. The products may also be used in  
 CC gene therapy protocols. The nucleic acids encoding signal peptides can be  
 CC used for directing extracellular secretion of a polypeptide or the  
 CC insertion of a polypeptide into a membrane, or importing a polypeptide  
 CC into a cell. The proteins encoded by the EST sequences may be useful in  
 CC treating a variety of human conditions. Secreted proteins have  
 CC therapeutic value, and the identification of new secreted proteins is  
 CC valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 68 AA:  
 Query Match 49.3%; Score 344; DB 21; Length 68;  
 Best Local Similarity 100.0%; Pred No. 9.8e-34;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHFLRFIVEFYLMGLTGAQRORKEESTEVKTEVLHREPCSKTSKKGDLNAHYDGYL 60  
 Db 5 mhflrfivffiywglftagrqkkestevklevlhrpencsktskkgdlnahdygl 64  
 QY 61 AKDG 64  
 Db 65 AKDG 68  
 RESULT 9  
 AAM87744  
 ID AAM87744 standard; Protein; 57 AA.  
 XX  
 AC AAM87744;  
 XX  
 DT 01-MAR-1999 (first entry)  
 XX  
 DE Secreted protein encoded by gene 23 clone HSOE084.  
 XX  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; testostosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9854963-A2.  
 XX  
 PD 10-DEC-1998.

XX  
 PF 04-JUN-1998; 98WO-US11422.  
 XX  
 PR 18-DEC-1997; 97US-0070923.  
 PR 06-JUN-1997; 97US-0048877.  
 PR 06-JUN-1997; 97US-0048881.  
 PR 06-JUN-1997; 97US-0048884.  
 PR 06-JUN-1997; 97US-0048893.  
 PR 06-JUN-1997; 97US-0048896.  
 PR 06-JUN-1997; 97US-0048899.  
 PR 06-JUN-1997; 97US-0048915.  
 PR 06-JUN-1997; 97US-0048949.  
 PR 06-JUN-1997; 97US-0048964.  
 PR 06-JUN-1997; 97US-0048972.  
 PR 06-JUN-1997; 97US-0049020.  
 PR 06-JUN-1997; 97US-0049375.  
 PR 05-SEP-1997; 97US-0057628.  
 PR 05-SEP-1997; 97US-0057635.  
 PR 05-SEP-1997; 97US-0057644.  
 PR 05-SEP-1997; 97US-0057647.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057661.  
 PR 05-SEP-1997; 97US-0057667.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 05-SEP-1997; 97US-0057764.  
 PR 05-SEP-1997; 97US-0057770.  
 PR 05-SEP-1997; 97US-0057775.  
 PR 05-SEP-1997; 97US-0057778.  
 PR 06-JUN-1997; 97US-0048875.  
 PR 06-JUN-1997; 97US-0048878.  
 PR 06-JUN-1997; 97US-0048882.  
 PR 06-JUN-1997; 97US-0048885.  
 PR 06-JUN-1997; 97US-0048894.  
 PR 06-JUN-1997; 97US-0048897.  
 PR 06-JUN-1997; 97US-0048900.  
 PR 06-JUN-1997; 97US-0048916.  
 PR 06-JUN-1997; 97US-0048962.  
 PR 06-JUN-1997; 97US-0048970.  
 PR 06-JUN-1997; 97US-0048974.  
 PR 06-JUN-1997; 97US-0049373.  
 PR 05-SEP-1997; 97US-0057654.  
 PR 05-SEP-1997; 97US-0057658.  
 PR 05-SEP-1997; 97US-0057662.  
 PR 05-SEP-1997; 97US-0057668.  
 PR 05-SEP-1997; 97US-0057762.  
 PR 05-SEP-1997; 97US-0057765.  
 PR 05-SEP-1997; 97US-0057771.  
 PR 05-SEP-1997; 97US-0057776.  
 PR 06-JUN-1997; 97US-0048876.  
 PR 06-JUN-1997; 97US-0048880.  
 PR 06-JUN-1997; 97US-0048886.  
 PR 06-JUN-1997; 97US-0048892.  
 PR 06-JUN-1997; 97US-0048895.  
 PR 06-JUN-1997; 97US-0048898.  
 PR 06-JUN-1997; 97US-0048901.  
 PR 06-JUN-1997; 97US-0048917.  
 PR 06-JUN-1997; 97US-0048963.  
 PR 06-JUN-1997; 97US-0048971.  
 PR 06-JUN-1997; 97US-0049019.  
 PR 06-JUN-1997; 97US-0049374.  
 PR 05-SEP-1997; 97US-0057627.  
 PR 05-SEP-1997; 97US-0057634.  
 PR 05-SEP-1997; 97US-0057643.  
 PR 05-SEP-1997; 97US-0057646.  
 PR 05-SEP-1997; 97US-0057649.  
 PR 05-SEP-1997; 97US-0057654.  
 PR 05-SEP-1997; 97US-0057666.  
 PR 05-SEP-1997; 97US-0057760.  
 PR 05-SEP-1997; 97US-0057763.



PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085689.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086023.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 28-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087098.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 30-JUL-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.

## (GETH ) GENENTECH INC.

PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 PI WPI: 1999-551358/46.  
 DR N-PSDB; AAX34013.

PT New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders -

PS Claim 12; Fig 53; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AAX33891 to  
 CC AAX24338, and AAY1465 to AAY1774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

CC Sequence 211 AA;

Query Match 38.9%; Score 271.5; DB 20; Length 211;  
 Best Local Similarity 44.2%; Pred. No. 2.1e-24;  
 Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

QY 3 FLFRIVFVYLMGLTQAOROKKESTEVKIEVLRHPKSCSTKSGLLAHNYGLAK 62  
 DB 4 flmaavilflvsligalipe-----pevklevlqkplchtkgqdlmlyhyegylek 58  
 QY 63 DSKRFYCGRTONEGHPKRVFVGVGVINGLDIAMTDMCGEGRKRVVIPPSPAYGKEGYDK 122  
 DB 59 dgsifshchkhngqpiwflgtlglealkywdqgikgmvcgkrrklilppalgygkegkqk 118

## RESULT 11

AY01458 standard; Protein; 211 AA.

AY01458;

18-MAY-1999 (first entry)

Polypeptide fragment encoded by gene 19.

Human; secreted protein; gene therapy; protein therapy; cancer; weight;  
 tumour; chromosome mapping; forensic; hematological disease; allergy;  
 inflammation; cell proliferation; viral infection; wound healing;  
 modulation; appetite; behaviour; food additive; preservative.

Homo sapiens.

WO9903990-A1.

28-JAN-1999.

15-JUL-1998; 98WO-US14613.

18-AUG-1997; 97US-0056361.  
 16-JUL-1997; 97US-0052661.  
 16-JUL-1997; 97US-0052870.  
 16-JUL-1997; 97US-0052871.  
 16-JUL-1997; 97US-0052872.  
 16-JUL-1997; 97US-0052873.  
 16-JUL-1997; 97US-0052874.  
 16-JUL-1997; 97US-0052875.  
 22-JUL-1997; 97US-0053440.  
 22-JUL-1997; 97US-0053441.  
 22-JUL-1997; 97US-0053442.  
 18-AUG-1997; 97US-0055683.  
 18-AUG-1997; 97US-0055724.  
 18-AUG-1997; 97US-0055725.  
 18-AUG-1997; 97US-0055726.  
 18-AUG-1997; 97US-0055946.  
 18-AUG-1997; 97US-0055952.  
 18-AUG-1997; 97US-0055985.  
 18-AUG-1997; 97US-0055989.  
 18-AUG-1997; 97US-0056359.

(HOMA-) HUMAN GENOME SCI INC.

Duan R, Feng P, Ferrle AM, Florence KA, Fouad J;  
 Greene JM, Hu J, Ni J, Rosen CA, Ruben SM, Young PE;  
 Yu G;

WPI: 1999-132234/11.  
 N-PSDB: AAX22229.

New nucleic acids encoding secreted human proteins - potentially  
 useful for treating and diagnosing diseases and identifying specific  
 binding agents

Disclosure; Page 21; 251pp; English.

The invention relates to nucleic acid sequences (AAX2221 to AAX22282)  
 encoding human secreted proteins (AAY01383 to AAY01454). The secreted  
 protein gene sequences are deposited with the ATCC under deposit number  
 ATCC 209138, 209139 or 209141. Host cells containing vectors comprising  
 the nucleic acid sequences are used for the recombinant expression of  
 the secreted proteins. The polynucleotide and amino acid sequences are  
 useful for preventing, treating or ameliorating medical conditions e.g.  
 by protein or gene therapy. Pathological conditions can be also diagnosed  
 by determining the amount of the new polypeptides in a sample or by the  
 presence of mutations in the new polynucleotides. The nucleic acid  
 sequences, or its fragments, are useful for chromosome identification  
 and mapping; as antisense and triplex-forming therapeutics; in gene  
 therapy; for (forensic) identification of individuals; as molecular  
 weight markers; to identify related sequences or specific mRNA; in  
 preparation of oligomers and to raise anti-DNA antibodies. Antibodies are  
 useful as immunoassay reagents (including for in vivo imaging) and  
 therapeutically to inhibit or activate particular polypeptides. A very  
 wide range of disorders may be treated with the polynucleotide and  
 polypeptide sequences, e.g. autoimmune or hematological diseases,  
 allergy, inflammation, cancer or other forms of cell proliferation, viral  
 or other infections. The sequences may also be useful in wound healing,  
 to modulate differentiation of embryonic stem cells, to modulate weight,

CC appetite, behaviour etc. and as food additive or preservative. The  
CC present sequence represents a polypeptide fragment encoded by a gene  
CC of the invention (see descriptor line for gene number).

XX Sequence 211 AA.

Query Match 38.9%; Score 271.5; DB 20; Length 211;  
Best Local Similarity 44.2%; Pred. No. 2,1e-24;  
Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

QY 3 FLFRFVFFVLMGLFTFAQORKEESTEVKIEVLHREPCSKTSKGGDLNHHYDGLAK 62  
DB 4 flmnavllflfvtslgallpe-----pevklevlqkpfchrtkktgqdlmlvhyegylek 58  
QY 63 DGSKFYCSRTQNGHPKPFVILGVGVKIGDIAMTDMCGEKKRVVIPPSPFVYKGEYDK 122  
DB 59 dgsflfsthkhmgpwlftgllealkgwqgllkgmcvgekrklllppalgygkqgk 118

RESULT 12

ID AAB44262 standard; Protein; 211 AA.

XX AAB44262;

DT 08-FEB-2001 (first entry)

XX Human PRO381 (UNQ322) protein sequence SEQ ID NO:145.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;  
XX expressed sequence tag; detection; cancer.

XX Homo sapiens.

XX WO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000MO-US04341.

XX 08-MAR-1999; 99MO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 29-MAR-1999; 99US-0126773.  
PR 21-APR-1999; 99US-0130332.  
PR 28-APR-1999; 99US-0131445.  
PR 14-MAY-1999; 99US-0141037.  
PR 23-JUN-1999; 99US-0145698.  
PR 26-JUL-1999; 99US-0162506.  
PR 29-OCT-1999; 99MO-US28313.  
PR 30-NOV-1999; 99MO-US28551.  
PR 02-DEC-1999; 99MO-US28565.  
PR 16-DEC-1999; 99MO-US30095.  
PR 30-DEC-1999; 99MO-US31243.  
PR 30-DEC-1999; 99MO-US31274.  
PR 05-JAN-2000; 2000MO-US00219.  
PR 06-JAN-2000; 2000MO-US00277.  
PR 06-JAN-2000; 2000MO-US00376.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Geber H, Gerltisen ME;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
XX WPI: 2000-611443/58.  
XX N-PSDB: AAC78488.

PT Novel PRO polypeptides and polynucleotides used in detection methods,  
PT to target bioactive molecules to specific cells, and to modulate

PT cellular activities :

XX Claim 12; Fig 53; 636pp; English.

CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
CC sequence tag) sequences which encode secreted or transmembrane PRO  
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
CC activity. The polynucleotides and polypeptides can be used for detecting  
CC the presence of PRO polypeptides in samples, for linking bioactive  
CC molecules to cells and for modulating biological activities of cells,  
CC using the polypeptides for specific targeting. The polypeptide targeting  
CC can be used to kill the target cells, e.g. for the treatment of cancers.  
CC The polypeptide pairs provide specific targeting of bioactive molecules  
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
CC the isolation of the PRO polynucleotide sequences.

XX Sequence 211 AA;

Query Match 38.9%; Score 271.5; DB 21; Length 211;  
Best Local Similarity 44.2%; Pred. No. 2,1e-24;  
Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

QY 3 FLFRFVFFVLMGLFTFAQORKEESTEVKIEVLHREPCSKTSKGGDLNHHYDGLAK 62  
DB 4 flmnavllflfvtslgallpe-----pevklevlqkpfchrtkktgqdlmlvhyegylek 58  
QY 63 DGSKFYCSRTQNGHPKPFVILGVGVKIGDIAMTDMCGEKKRVVIPPSPFVYKGEYDK 122  
DB 59 dgsflfsthkhmgpwlftgllealkgwqgllkgmcvgekrklllppalgygkqgk 118

RESULT 13

ID AAB24021 standard; Protein; 211 AA.

XX AAB24021;

DT 25-JAN-2001 (first entry)

XX Human PRO381 protein sequence SEQ ID NO:2.

KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;  
XX identification; tumorigenesis; anticancer; detection.

XX Homo sapiens.

XX WO200053750-A1.

PD 14-SEP-2000.

XX 02-DEC-1999; 99MO-US28551.  
XX 08-MAR-1999; 99MO-US05028.  
PR 01-SEP-1999; 99MO-US20111.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99MO-US28313.  
PR 01-DEC-1999; 99MO-US28634.

XX (GETH ) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;  
PI WPI: 2000-594320/56.  
PI N-PSDB: AAC58103.

PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
PT the growth of tumors in mammals, and to identify inhibitors of PRO  
PT polypeptide activity or expression -

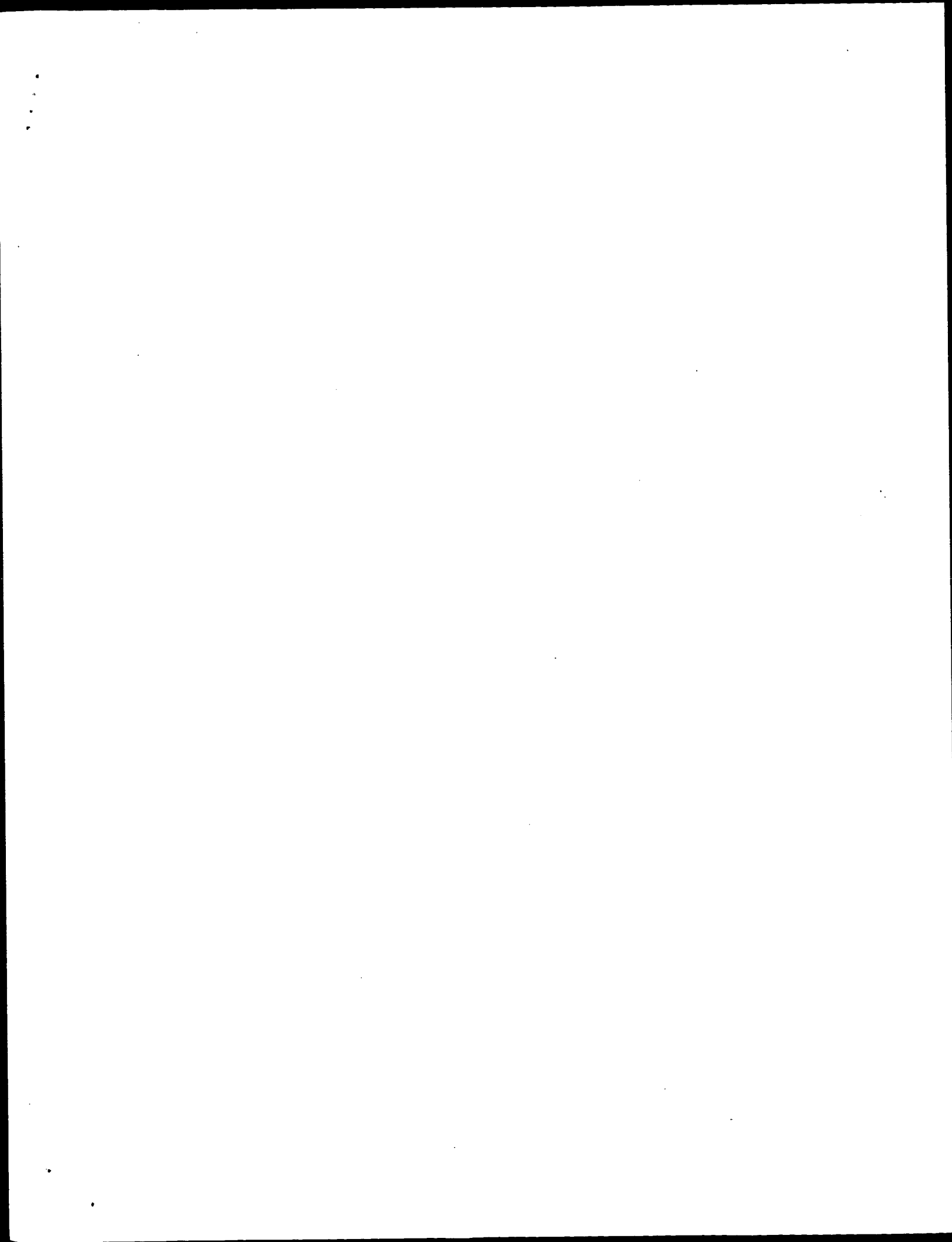
XX Claim 61; Fig 2; 226pp; English.

XX The present invention describes an antibody that binds to a human











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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:05 ; Search time 12.42 Seconds

(without alignments)  
213.861 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 1 MHFLFRFVFLMGLTAAQ.....PPSAVYKGYDKPLAKGI 129

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 197339 segs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/6C\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199.5	28.6	141	1	US-07-822-966B-6
2	199.5	28.6	142	1	US-08-336-618-18
3	199.5	28.6	142	5	PCT-US92-03993-7
4	197.5	28.3	99	5	PCT-US92-03993-5
5	190	27.2	582	2	US-08-989-386-1
6	188.5	27.0	141	2	US-08-803-899-6
7	182	26.1	581	2	US-08-989-386-7
8	178.5	25.6	105	4	US-08-894-173-84
9	178.5	25.6	105	4	US-09-398-193-84
10	176.5	25.3	135	1	US-08-336-618-20
11	163.5	23.4	88	1	US-08-336-618-19
12	157.5	22.6	104	3	US-08-894-173-86
13	157.5	22.6	104	4	US-09-398-193-86
14	144	20.6	107	3	US-08-894-173-66
15	144	20.6	107	4	US-08-894-173-79
16	144	20.6	107	3	US-09-398-193-66
17	144	20.6	107	4	US-09-398-193-79
18	144	20.6	107	3	US-09-398-193-66
19	144	20.6	107	4	US-09-398-193-79
20	142	20.3	107	3	US-08-336-618-16
21	142	20.3	107	3	US-08-894-173-69
22	142	20.3	107	4	US-08-894-173-83
23	142	20.3	107	4	US-09-398-193-83
24	142	20.3	119	5	PCT-US92-03993-1
25	142	20.3	120	1	US-08-336-618-17
26	139.5	20.0	164	2	US-08-803-899-7
27	138.5	19.8	145	1	US-08-336-618-21

28	135.5	19.4	108	2	US-08-803-899-2	Sequence 2, Appli
29	135.5	19.4	108	2	US-08-803-899-5	Sequence 5, Appli
30	135.5	19.4	411	2	US-08-741-134-6	Sequence 6, Appli
31	133	19.1	107	1	US-08-197-795-2	Sequence 2, Appli
32	133	19.1	107	1	US-08-336-618-15	Sequence 2, Appli
33	133	19.1	107	5	PCT-US92-03993-3	Sequence 15, Appli
34	133	19.1	107	5	PCT-US92-03993-3	Sequence 3, Appli
35	131.5	18.8	103	5	US-08-894-173-85	Sequence 2, Appli
36	131.5	18.8	103	4	US-09-398-193-85	Sequence 85, Appli
37	131	18.8	458	1	US-08-336-618-24	Sequence 85, Appli
38	130.5	18.7	108	2	US-08-803-899-4	Sequence 24, Appli
39	130	18.6	104	3	US-09-012-515A-6	Sequence 4, Appli
40	130	18.6	104	4	US-08-360-144A-6	Sequence 6, Appli
41	130	18.6	104	5	PCT-US95-06722-6	Sequence 6, Appli
42	130	18.6	107	1	US-08-336-618-13	Sequence 6, Appli
43	130	18.6	107	2	US-08-963-601-1	Sequence 13, Appli
44	130	18.6	107	2	US-08-744-701-7	Sequence 1, Appli
45	130	18.6	107	3	US-08-894-173-67	Sequence 7, Appli

#### ALIGNMENTS

RESULT 1

US-07-822-966B-6

Sequence 6, Application US/07822966B

Patent No. 5498597

GENERAL INFORMATION:

APPLICANT: Steven J. Burakoff

APPLICANT: Barbara E. Bierer

TITLE OF INVENTION: FKBP-13, AN FK506-BINDING

TITLE OF INVENTION: IMMUNOPHILIN

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/822, 966B

FILING DATE: January 17, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 00530/052001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 141 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-822-966B-6

Query Match

Best Local Similarity 28.6%; Score 199.5; DB 1; Length 141;

Matches 44; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

26 ESTEEVKTEVLRHRENCSTKSGKGLNNAHYDGLYARDGSKFYCSPTNONGCHPKWFLGV 85



```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
TELEFAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03993-5

```

```

Query Match      28.3%; Score 197.5; DB 5; Length 99;
Best Local Similarity 46.8%; Pred. No. 8.5e-17;
Matches 44; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

```

```

QY 26 ESTEEVIEVLHREPCSKTSKGGDLINAHYDGLAKDSKFCSTQNGHGRKWEVLGY 85
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 4 EGGKGLDYGKRRKVDHCPISRKGDVLMHMYTKL-EDGTEFDSLPQNO--PFVESLGT 60
QY 86 GOVYKGLDIAMTDMPCEKRRVYIPSPFAYGKEG 119
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 61 GOVYKGMDOGLGMCBEGERKRLVYIPSELGGERG 94

```

```

RESULT 5
US-08-989-386-1
; Sequence 1, Application US/08989386
; Patent No. 5989860
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0443 US

```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVARUT01
CLONE: 2255114
US-08-989-386-1

```

```

Query Match      27.2%; Score 190; DB 2; Length 582;
Best Local Similarity 35.0%; Pred. No. 8.3e-15;
Matches 41; Conservative 26; Mismatches 36; Indels 14; Gaps 4;

```

```

QY 4 LRFETVFEYLNLGFTAKORKEESTEEVIEVLHREPCSKTSKGGDLINAHYDGLAKD 63
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 140 LYFDVLLDVG-----NKEDT---VQVSTLRPHPCPRWVODGFVRHYNGTLL-D 187
QY 64 GSKFYCSRTQNGHPKWEVLGVGOVYKGLDIAMTDMPCEKRRVYIPSPFAYGKEGY 120
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 188 GTSFDTSYSGKGTIDY--VGSGLIKGMDGLGMCBEGERKRLIIPPLAYGEGY 242

```

```

RESULT 6
US-08-803-899-6
; Sequence 6, Application US/08803899
; Patent No. 5912224
; GENERAL INFORMATION:
; APPLICANT: DONAHUE, PATRICIA K.
; APPLICANT: WANG, TONGWEN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,899
; FILING DATE: 02/21/1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/012,054
; FILING DATE: 02/22/1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: STERFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609,4240001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-803-899-6

Query Match	27.0%;	Score 188.5;	DB 2;	Length 141;
Best Local Similarity	45.7%;	Pred. No. 1.8e-15;		
Matches 43;	Conservative 15;	Mismatches 33;	Indels 3;	Gaps 2

[illegible]

RESULT 7  
US-08-989-386-7

; Sequence 7, Application US/08989386  
; Patent No. 5989860  
GENERAL INFORMATION.

1 GENERAL INFORMATION:  
2 APPLICANT: Bandman, Olga  
3 APPLICANT: Hillman, Jennifer L.  
4 APPLICANT: Guegler, Karl J.  
5 APPLICANT: Corley, Neil C.  
6 APPLICANT: Shah, Purvi  
7 TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS  
8 NUMBER OF SEQUENCES: 9  
9 CORRESPONDENCE ADDRESS:

ADDRESS: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94504  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/989,386  
FILING DATE:

CLASSIFICATION: \_\_\_\_\_  
PRIOR APPLICATION DATA: \_\_\_\_\_  
APPLICATION NUMBER: \_\_\_\_\_  
FILING DATE: \_\_\_\_\_  
ATTORNEY/AGENT INFORMATION: \_\_\_\_\_  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0443 US  
TELECOMMUNICATION INFORMATION: \_\_\_\_\_  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX: \_\_\_\_\_  
INFORMATION FOR SEQ ID NO: 7:

? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 581 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? IMMEDIATE SOURCE:  
 ? LIBRARY: GenBank  
 ? CLONE: 894162  
 US-08-989-386-7

	Query Match	26.1%;	Score 182;	DB 2;	Length 581;
	Best Local Similarity	37.9%;	Pred. No. 7.8e-14;		
	Matches	39;	Conservative	24;	Mismatches 30;
					Indels 10;
					Gap
QY	28 TREVITETVLRH-PENCSTKSKGDLNAAHYDGLAKSGKFYCSPFQNGCHPKWFLVG	8			

Db 376 SDPVEIKTLSPENCNETSKIGDFIRHYNCSSL-DGTRLFSSHDYEA--PQETTLGAN 432

```
07 QVTKGLDIAMTMCPEGRKRVVIPSPAYGKEGYDKRLLAKGI 122
   :|::||: |::|:||||:| ||: |
Db 433 KVIEGLDRLOGMCGVERQLIVPHLAHGNG-----ARCV 468
```

RESULT	8
US-08-894-173-84	

```

; Sequence 84: Application US/0003473A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylylate cyclase and uses thereof
; FILE REFERENCE: P14/716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ. ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;
; LENGTH: 105
; TYPE: prt
; ORGANISM: Human
US-08-894-173-84

```

Query Match	25.68;	Score 178.5;	DB 3;	Length 105;
Best Local Similarity	48.88;	Pred. No. 1.9e-14;		
Matches 40;	Conservative 12;	Mismatches 27;	Indels 3;	Gaps 2;

[illegible]

```

; RESULT 9
; US-09-398-193-84
; Sequence 84: Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylylate cyclase and uses thereof
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
; US-09-398-193-84

```

Query Match	25.6%	Score 178.5	DB 4	Length 105
Best Local Similarity	48.8%	Pred. No. 1.9e-14		
Matches 40	Conservative 12	Mismatches 27	Indels 3	Gaps 2
QY	38	REPENSKTSKKGDLINAHYDGYLAKGSKRKYCRNQNEGHPKFWILGAGVYIKGDIAMT	97	
DB	1	RVDHPIKSRKGDVLAHHHTYGL-EIDSTEDSSLPNO--PFVSLGCGVYIKKMDGDL	57	

```

QY      98 DMCPEGKRRVYIPPSFAYGKEG 119
          | | | | | | | |
          58 GMYEGEKRRKLYIPSLGSGERG 79

RESULT 10
US-08-336-618-20

```

```

1 APPLICANT: Harding, Matthew W.
2 APPLICANT: Livingston, David J.
3 TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
4 TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
5 TITLE OF INVENTION: GNA
6 NUMBER OF SEQUENCES: 32
7 CORRESPONDENCE ADDRESS:
8 ADDRESS: Hamilton, Brook, Smith and Reynolds, P.C.
9 STREET: Two Millitia Drive
10 CITY: Lexington
11 STATE: Massachusetts
12 COUNTRY: U.S.A.
13 ZIP: 02173
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/336,618
23 FILING DATE: 09-NOV-1994
24 CLASSIFICATION: 435
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 07/963,325
28 FILING DATE: 16-OCT-1992
29 APPLICATION NUMBER: US 07/777,752
30 FILING DATE: 11-OCT-1991
31
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: PCT/
34 FILING DATE: 09-OCT-1992
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Granahan, Patricia
37 REGISTRATION NUMBER: 32,227
38 REFERENCE/DOCKET NUMBER: VP191-06A
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 617-861-6240
41 TELEFAX: 617-861-9540
42 INFORMATION FOR SEQ ID NO: 19:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 88 amino acids
45 TYPE: amino acid
46 TOPOLOGY: linear
47
48 MOLECULE TYPE: protein
49
50 US-08-336-618-19

```

[illegible]

; TYPE: PRT  
 ; ORGANISM: Yeast  
 US-08-894-173-86

Query Match	22.6%	Score 157.5;	DB 3;	Length 104;
Best Local Similarity	45.0%;	Pred. No. 7.1e-12;		
Matches 36;	Conservative 11;	Mismatches 30;	Indels 3;	Gaps 2

```

Oy 40 ENCSTSKKGLLNAHYDGLYAKDSDKFCYCSRTQNEGHPKWEVLGVGVQVLIKGLDINTDM 99
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 7 EDCLIKAMPGDVKVHYHTGSL-ESGTF--DSSYSRSGPIAEFLGCGRAIVKIGWDQGVAGM 63

```

```
QY 100 CPGEKRRKVIPPSEAYGKEG 119
      | | | | | : | | | | | : |
Db 64 CVGEKRRKLQIPSSLAYGERG 83
```

```

, RESULT 13
US-09-398-193-86
, Sequence 86, Application US/09398193
, Patent No. 6197581
, GENERAL INFORMATION:
, APPLICANT: Medical Research Council
, TITLE OF INVENTION: Adenylylate cyclase and uses therefor
, FILE REFERENCE: P24360-
, CURRENT APPLICATION NUMBER: US/09/398,193
, CURRENT FILING DATE: 1999-09-17
, NUMBER OF SEQ ID NOS: 104
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 86
, LENGTH: 104
, TYPE: PRT
, ORGANISM: Yeast
US-09-398-193-86

```

Query Match	22.68;	Score 157.5;	DB 4;	Length 104;
Best Local Similarity	45.08;	Pred. No. 7.1e-12;		
Matches	36;	Conservative	11;	Mismatches 30;
				Indels 3;
				Gaps 2

Qy 40 ENCSKTSKKGDLNAHYDGLAKDGSKFYCSRTQNKGHPKFVLGVGGVATKGLDIMTDM 99  
| : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 7 EDCLIKAMPGDVKVHYTGSL-ESGYE--DSYSRSGSDIAFELGVGRVIKGMDDGVAGM 63

```
QY 100 CPGEKRKVVIPPSFAYGKEG 119
      | | | | | : | | | | | : |
DB 64 CVGEKRKLQIPSSLAYGERG 83
```

```

US-08-894-173-66
RESULT 14
US-08-894-173-66
Sequence 66, Application US/08894173A
Patent No. 6090612
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and
FILE REFERENCE: P14716C
CURRENT APPLICATION NUMBER: US/08/894,173A
CURRENT FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 107
TYPE: prt
ORGANISM: Saccharomyces cerevisiae
US-08-894-173-66

```

Query Match	20.6%	Score 144;	DB 3;	Length 107;
Best Local Similarity	38.9%;	Pred. No. 3.3e-10;		
Matches 35; Conservative	17;	Mismatches 34;	Indels 4;	Gaps 3

[illegible]

```

; RESULT 15
; US-08-894-173-79
; Sequence 79, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Yeast
; US-08-894-173-79

```

Query Match	20.68	Score 144	DB 3	Length 107
Best Local Similarity	38.98	Pred. No. 3	3e-10	
Matches	35	Conservative	17	Mismatches 34
				Indels 4
				Gaps 3

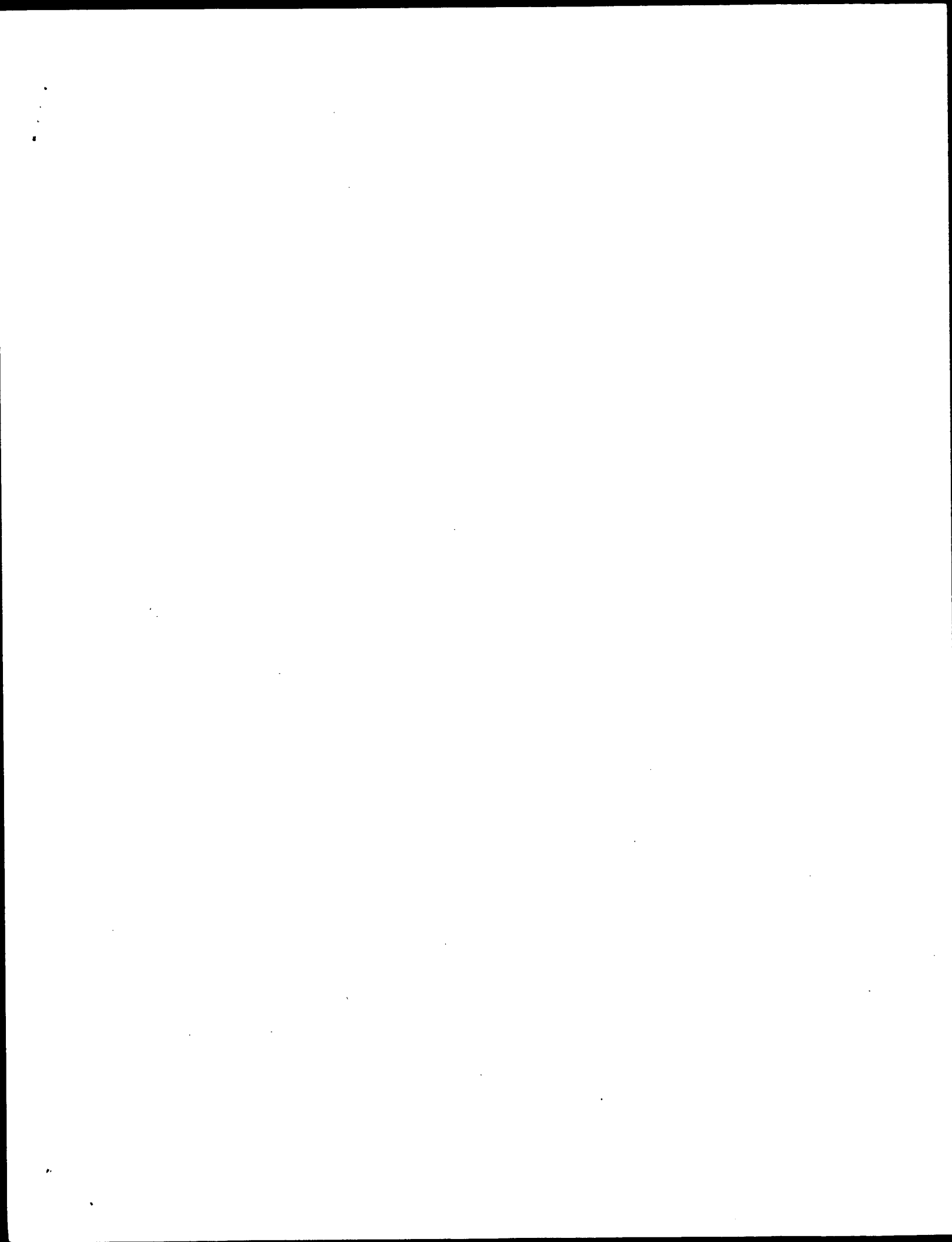
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QY      31 VKIETLHRENGCKSTKSGGLLAHNDGYLADDSKFCFSTONEGHPKMFVIGVCQIK 90
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      2 VKIDIT-SFGDGAFFPTGDLVITHTGL-ENGCK--DSVDGSPGQONIGVGQIK 57
QY      91 GIDITMDMCGEGRKKVIPPSPARKBEY 120
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      58 GMDVGIPKLIVGEKARLLITGPATVGRPF 87

```

Search completed: August 31, 2001, 12:05:50  
Job time: 105 sec







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:05 ; Search time 14.47 seconds  
(without alignments)  
679.096 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLRFYFYVGLMGLTAQ.....PPSFAYGKGYDKPLAKGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	205.5	29.4	139	T21882	hypothetical prote
2	204.5	29.3	261	T31741	hypothetical prote
3	199.5	28.6	140	I49668	binding protein -
4	199.5	28.6	142	JC1365	FK506/rapamycin-bi
5	186.5	26.7	163	S71238	probable peptidylp
6	182	26.1	581	I49669	FKBP65 binding pro
7	180	25.8	151	T12090	probable peptidylp
8	178.5	25.6	146	S71237	probable peptidylp
9	178	25.5	134	UT0748	FK506-binding prot
10	176.5	25.3	135	S25337	probable peptidylp
11	175	25.1	262	T42709	peptidylprolyl iso
12	172.5	24.7	264	T29780	hypothetical prote
13	158.5	22.7	259	T27586	hypothetical prote
14	153.5	22.0	201	S75144	hypothetical prote
15	147.5	22.0	124	JN0320	FKBP-type peptidyl
16	145	20.8	132	B75347	rapamycin-binding
17	144	20.6	114	A33146	peptidyl-prolyl ci
18	142.5	20.4	215	A40050	peptidylprolyl iso
19	142.5	20.4	392	S55971	probable peptidylp
20	142	20.3	120	S11090	FK506-binding prot
21	141	20.2	551	S72485	peptidylprolyl iso
22	139.5	20.0	105	M40211	FK506-inhibitable
23	139.5	20.0	224	JU01522	peptidylprolyl iso
24	137.5	19.7	487	T10215	hypothetical prote
25	135.5	19.4	108	S54139	FK506-binding prot
26	135.5	19.4	411	S48647	peptidylprolyl iso
27	134	19.2	559	S55383	peptidylprolyl iso
28	133.5	19.1	109	B20222	peptidylprolyl iso
29	133.5	19.1	109	F81245	FKBP-type peptidyl

30	133	19.1	107	2	A61431	peptidylprolyl iso
31	132.5	19.0	457	2	JC5422	FK506-binding prot
32	131	18.8	458	1	A42386	hsp 90-binding pro
33	130	18.6	108	2	A35780	peptidylprolyl iso
34	130	18.6	108	2	A42657	FK506-binding prot
35	129.5	18.6	412	2	A55320	immunophilin FKBP4
36	128.5	18.4	112	2	T40724	peptidyl-prolyl ci
37	128.5	18.4	357	2	JC4090	FK506-binding 39k
38	128	18.3	568	2	T06489	probable peptidylp
39	124	17.8	108	2	JH0528	FK506-binding prot
40	124	17.8	123	1	A43328	peptidylprolyl iso
41	124	17.8	458	2	JN0873	immunophilin p59 -
42	123.5	17.7	79	2	S39850	FKBP immunophilin
43	122.5	17.6	240	2	A64403	peptidylprolyl iso
44	122	17.5	459	2	A46372	immunophilin FKBP5
45	120	17.2	159	2	T46954	peptidylprolyl iso

#### ALIGNMENTS

RESULT 1

T21882

hypothetical protein F36H1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000

C:Accession: T21882

R:Kershaw, J.

submitted to the EMBL Data Library, January 1996

A:Reference number: 219482

A:Accession: T21882

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-139 <M13>

A:Cross-references: EMBL:Z68760; PIDN:CAA92994.1; GSPDB:GN00022; CESP:F36H1.1

A:Experimental source: clone F36H1

C:Genetics:

A:Gene: CESP:F36H1.1

A:Map position: 4

A:Introns: 43/2: 80/3

C:Superfamily: BkBP-type peptidylprolyl isomerase; BkBP-type peptidylprolyl isomerase F:45-92/Domain: BkBP-type peptidylprolyl isomerase homology <PPI>

Query Match 29.4%; Score 205.5; DB 2; Length 139;  
Best Local Similarity 46.3%; Pred. No. 4.7e-13;  
Matches 44; Conservative 16; Mismatches 32; Indels 3; Gaps 2;

OY 25 ESTEVEKIEVLAHPNCSKTSKGGDLNAHYDGLAKDSKFCYCSRTONGHKKWVLG 84

DB 21 ECKIDKLDIGVKKRAENCVRKSGDQLMHMYTGTL-DGTEFDSSTRNEET--FTLG 77

OY 85 VGVVTKGLDIAMTDMCPGCKRRVYIPPSFAYGKGG 119

DB 78 QGNVTKGMDGLNKCVRERILITPPLGTCGNG 112

RESULT 2

T31741

hypothetical protein C05C8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 02-Sep-2000

C:Accession: T31741

R:Sammons, L.; Wohlmann, P.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid C05C8.

A:Reference number: 221078

A:Accession: T31741

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-261 <SAM>

A:Cross-references: EMBL:AF016430; PIDN:AA865370.1; GSPDB:GN00023; CESP:C05C8.3

A:Experimental source: strain Bristol N2; clone C05C8

C:Genetics:  
 A:Gene: CESP:C05C8.3  
 A:Map position: 5  
 A:Introns: 119/3  
 C:Superfamily: BKB-type peptidylprolyl isomerase homology <PPI>  
 F:48-94/Domain: BKB-type peptidylprolyl isomerase homology <PPI2>  
 F:166-213/Domain: BKB-type peptidylprolyl isomerase homology <PPI2>

Query Match 29.3%; Score 204.5; DB 2; Length 261;  
 Best Local Similarity 44.5%; Pred. No. 1.2e-12;  
 Matches 49; Conservative 15; Mismatches 43; Indels 3; Gaps 2;

QY 10 FFYLMGLFTAQROKKESTEVEKIEVLHREPCSKTKGDLNNAHYDGLAKDGSFKFC 69  
 DB 127 FVELKSTIFRKPQAKWITDEGVHITHEVEGCTEKRAQAGDTLHQOYTLNL-EDGSFIDS 185

QY 70 SRQNGHPRKFWFLVGVYKGLDIAMTDMCPGKKRVVIPPSPFAYGKEG 119  
 DB 186 SMSRN--RPEIFRMGSGQVYKGMIDMEGMCQGEKKRVVIPPSPFAYGENG 233

RESULT 3  
 149668  
 binding protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I49668  
 R:Hendrickson, B.A.; Zhang, W.; Craig, R.J.; Jin, Y.  
 Gene 134, 271-275, 1993  
 A:Title: Structural organization of the genes encoding human and murine FK506-binding pr  
 A:Reference number: I49668; MUID:94085790  
 A:Accession: I49668  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-140 <RES>  
 A:Cross-references: GB:M7831; NID:q433782; PIDN:AAA7631.1; PID:q433783  
 C:Genetics:  
 A:Gene: FKBP13  
 A:Introns: 55/3; 93/2; 109/1; 121/1  
 C:Superfamily: BKB-type peptidylprolyl isomerase; BKB-type peptidylprolyl isomerase ho  
 F:47-94/Domain: BKB-type peptidylprolyl isomerase homology <PPI>

Query Match 28.6%; Score 199.5; DB 2; Length 140;  
 Best Local Similarity 46.8%; Pred. No. 1.8e-12;  
 Matches 44; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

QY 26 ESTEEVKIEVLHREPCSKTKGDLNNAHYDGLAKDGSFKFCSTQNGHPRKFWFLGV 85  
 DB 24 EGKRLQIGVKKRVDPCHPIKSRKGDVLMHNTGKL-EDGTEFDSLSLPQNG--PFVPSLGT 80

QY 86 GOVYKGLDIAMTDMCPGKKRVVIPPSPFAYGKEG 119  
 DB 81 GOVYKGMDOGLGMCCEGKKRLVIPPSELGYGEG 114

RESULT 4  
 JC1365  
 FK506/rapamycin-binding protein FKBP13 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-Aug-1998  
 C:Accession: JC1365; A39602  
 R:Dilella, A.G.; Hawkins, A.; Craig, R.J.; Schreiber, S.L.; Griffin, C.A.  
 Biochem. Biophys. Res. Commun. 189, 819-823, 1992  
 A:Title: Chromosomal band assignments of the genes encoding human FKBP12 and FKBP13.  
 A:Reference number: JC1365; MUID:93112052  
 A:Accession: JC1365  
 A:Molecule type: DNA  
 A:Residues: 1-142 <DL>  
 R:Jin, Y.J.; Albers, M.W.; Lane, W.S.; Blierer, B.E.; Schreiber, S.L.; Burakoff, S.J.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6677-6681, 1991  
 A:Title: Molecular cloning of a membrane-associated human FK506- and rapamycin-binding p

A:Reference number: A39602; MUID:91319747

A:Accession: A39602  
 A:Molecule type: mRNA  
 A:Residues: 1-20, 5'123-142 <JIN>  
 A:Cross-references: GB:M65128  
 C:Genetics:

A:Gene: GDB:FKBP2  
 A:Cross-references: GDB:133728; OMIM:186946  
 A:Map position: 11q13.1-11q13.3  
 A:Introns: 57/3; 95/2; 111/1; 123/1  
 C:Superfamily: BKB-type peptidylprolyl isomerase; BKB-type peptidylprolyl isomerase  
 C:Keywords: immunoregulation  
 F:1-22/Domain: signal sequence  
 F:23-142/Product: FK506/rapamycin-binding protein FKBP13 #status predicted <SIG>  
 F:49-96/Domain: BKB-type peptidylprolyl isomerase homology <PPI>

Query Match 28.6%; Score 199.5; DB 2; Length 142;  
 Best Local Similarity 46.8%; Pred. No. 1.9e-12;  
 Matches 44; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

QY 26 ESTEEVKIEVLHREPCSKTKGDLNNAHYDGLAKDGSFKFCSTQNGHPRKFWFLGV 85  
 DB 26 EGKRLQIGVKKRVDPCHPIKSRKGDVLMHNTGKL-EDGTEFDSLSLPQNG--PFVPSLGT 82

QY 86 GOVYKGLDIAMTDMCPGKKRVVIPPSPFAYGKEG 119  
 DB 83 GOVYKGMDOGLGMCCEGKKRLVIPPSELGYGEG 116

RESULT 5  
 S71238  
 probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-2 - Arabidopsis thaliana  
 N:Alternate names: FK-binding protein 15-2; Immunophilin  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: S71238  
 R:luan, S.; Kudla, J.; Grunsem, W.; Schreiber, S.L.  
 submitted to the EMBL Data Library, March 1996  
 A:Description: Molecular characterization of a FKBP-type immunophilin from higher pla  
 A:Reference number: S71238  
 A:Accession: S71238  
 A:Molecule type: mRNA  
 A:Residues: 1-163 <LUA>  
 A:Cross-references: EMBL:U52047; NID:q1272407; PIDN:AAC49391.1; PID:q1272408  
 C:Genetics:  
 A:Gene: FKBP15-2  
 C:Superfamily: BKB-type peptidylprolyl isomerase; BKB-type peptidylprolyl isomerase  
 C:Keywords: cis-trans-isomerase  
 F:52-99/Domain: BKB-type peptidylprolyl isomerase homology <PPI>

Query Match 26.7%; Score 186.5; DB 2; Length 163;  
 Best Local Similarity 36.6%; Pred. No. 4.1e-11;  
 Matches 49; Conservative 16; Mismatches 48; Indels 21; Gaps 5;

QY 7 FIVFYLMGL--FTAQROKKESTEVEKIEVLHREPCSKTKGDLNNAHYDGLAKD 64  
 DB 12 FLIFFLSLISLOGFA---KKTGVSPLQIGVKKRPTCEVQAHKDDITKVHNRGKIT-DG 66

QY 65 SKRYCSTQNGHPRKFWFLVGVYKGLDIAMTDMCPGKKRVVIPPSPFAYGKEG----- 119  
 DB 67 TVP--DSSFERGDPPEFKLGSGQVYKGMDOGLGACVGEKKRLKIPAKLIGEGSGSPPT 124

QY 120 -----YDKPILA 126  
 DB 125 PGATLIFPTELIA 138

RESULT 6  
 I49669  
 FKBP65 binding protein - mouse  
 C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I49669  
 R:Simsek, S.L.; Kozak, C.A.; Winterstein, D.; Hegamyer, G.; Colburn, N.H.  
 Genomics 18, 407-409, 1993  
 A>Title: Sequence and localization of a novel FK506-binding protein to mouse chromosome  
 A:Reference number: A48920; MUID:94117013

A:Accession: I49669  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-581 <RES>  
 A:Cross-references: GB:I07063; NID:9894161; PIDN:AAC37678.1; PID:9894162  
 C:Superfamily: BKBP-type peptidylprolyl isomerase homology  
 F:61-108/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>  
 F:173-220/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>  
 F:285-332/Domain: BKBP-type peptidylprolyl isomerase homology <PPI3>  
 F:398-445/Domain: BKBP-type peptidylprolyl isomerase homology <PPI4>

Query Match 26.1%; Score 182; DB 2; Length 581;  
 Best Local Similarity 37.9%; Pred. No. 4.4e-10;

Matches 39; Conservative 24; Mismatches 30; Indels 10; Gaps 4;

QY 28 TEKKIEVLNR-PENCSTKSKGDLNAHYDGYLAKDGFYCSRNQEGHPKMFVLGVG 86  
 Db 376 SDPEKILTSRPENCNETSKIDFTYHNCSL-DGTLFSSHYEA--PQETILGAN 432

QY 87 QVTKGDIAMTDMCPGKRRKRVIPSPFAYGKGYDKPLAKGI 129  
 Db 433 KVIEGIDRLGLOGMCGVGERROLIVPHLHAGENG-----ARGV 469

RESULT 7  
 T12090  
 Probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15 precursor - fava bean

N:Alternate names: FK506-binding protein; immunophilin; rapamycin-binding protein  
 C:Species: Vicia faba (fava bean)  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 21-Jul-2000  
 C:Accession: T12090

R:Luani, S.; Kudla, J.; Grisse, W.; Schreiber, S.L.  
 Proc. Natl. Acad. Sci. U.S.A. 93, 6964-6969, 1996

A>Title: Molecular characterization of a FKBP-type immunophilin from higher plants.  
 A:Reference number: Z17411; MUID:96293457

A:Accession: T12090

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-151 <LUA>

A:Cross-references: EMBL:U52045; NID:91272409; PIDN:AAC49392.1; PID:91272410

C:Genetics:

A:Gene: FKBP15

A>Note: Inhibited by immunosuppressant drugs FK506 and rapamycin

C:Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase hc

C:Keywords: cis-trans-isomerase; cyclosporin A binding; Immunoregulation

F:1-22/Domain: signal sequence #status predicted <SIS>

F:23-151/Product: peptidylprolyl isomerase FKBP15 #status predicted <MAT>

F:49-96/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 25.8%; Score 180; DB 2; Length 151;  
 Best Local Similarity 39.8%; Pred. No. 1.6e-10;

Matches 45; Conservative 14; Mismatches 48; Indels 6; Gaps 3;

QY 7 FTVFYLMGLFTAQRQKEESTEEVKIEVLHRENCSTKSKGDLNAHYDGYLAKDGSK 66  
 Db 10 FTFTIILALVNA---KSAADYTELQIGVKYKPPASCEVAAHGGDKVYHRRKLT-DGTV 65

QY 67 FICSRQNEGHKRWVVLGVGVIGKDIAMTDMCPGKRRKRVIPSPFAYGKEG 119  
 Db 66 FDSSEFRNS--PIDELGGGVYIKGWDGILGMCIGEKRRKLTIPAKLGYGEGG 116

RESULT 8  
 S71237  
 Probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-1 - Arabidopsis thaliana

N:Alternate names: FK-binding protein 15-1; immunophilin

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S71237

R:Luani, S.; Kudla, J.; Grisse, W.; Schreiber, S.L.

submitted to the EMBL Data Library, March 1996

A:Description: Molecular characterization of a FKBP-type immunophilin from higher pla

A:Reference number: S71237

A:Accession: S71237

A:Molecule type: mRNA

A:Residues: 1-146 <LUA>

A:Cross-references: EMBL:U52046; NID:91272405; PIDN:AAC49390.1; PID:91272406

C:Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase

C:Keywords: cis-trans-isomerase

F:45-92/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 25.6%; Score 178.5; DB 1; Length 146;  
 Best Local Similarity 38.2%; Pred. No. 2.2e-10;

Matches 42; Conservative 12; Mismatches 53; Indels 3; Gaps 2;

QY 10 FTYLMGLFTAQRQKEESTEEVKIEVLHRENCSTKSKGDLNAHYDGYLAKDGSFVC 69  
 Db 6 FLLTLITLTAAYKKSQDYTELQIGVKYKPKCDLQAHKDKIKVHNGKLT-DGTVF-- 62

QY 70 SFRQNEGHKRWVVLGVGVIGKDIAMTDMCPGKRRKRVIPSPFAYGKEG 119  
 Db 63 DSSFERKDPTEFELGIGVYIPWMDGILGACVGERKRLKIPSKLGYGNG 112

RESULT 9  
 J70748  
 FK506-binding protein - Botryllus schlosseri

C:Species: Botryllus schlosseri

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: J70748; S40074

R:Pancer, Z.; Gershon, H.; Rinkevich, B.

Biochem. Biophys. Res. Commun. 197, 973-977, 1993

A>Title: cDNA cloning of a putative protochordate FK506-binding protein.

A:Reference number: J70748; MUID:94092189

A:Accession: J70748

A:Molecule type: mRNA

A:Residues: 1-134 <PAN>

A:Cross-references: EMBL:X76006; NID:9435470; PIDN:CAA53594.1; PID:9435471

C:Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase

F:41-88/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 25.5%; Score 178; DB 1; Length 134;  
 Best Local Similarity 46.2%; Pred. No. 2.2e-10;

Matches 42; Conservative 13; Mismatches 32; Indels 4; Gaps 3;

QY 29 EYVKIEVLHRENCSTKSKGDLNAHYDGYLAKDGSFYSRNQEGHPKMFVLGVGV 88  
 Db 22 DKLQIGVLKRAVE-CERKSGSDVDMDHMTGFL-EDGSKFSSRRDRT--PTFTLGGGVY 77

QY 89 IKGLDIAMTDMCPGKRRKRVIPSPFAYGKEG 119  
 Db 78 IKGMKGLGMCIGEKRRKLTIPDMGYGDRG 108

RESULT 10  
 S25337  
 Peptidylprolyl isomerase (EC 5.2.1.8) FKBP precursor - yeast (Saccharomyces cerevisiae)

N:Alternate names: FK506-binding protein FKBP-13; protein YDR519w; rapamycin-binding

C:Species: Saccharomyces cerevisiae

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 16-Jul-1999

C:Accession: S25337; A46154; B46154; S69576

R:Partaledis, J.A.; Fleming, M.A.; Harding, M.W.; Berlin, V.

Yeast 8, 673-680, 1992

A>Title: Saccharomyces cerevisiae contains a homolog of human FKBP-13, a membrane-ass





Fri Aug 31 12:10:25 2001

us-09-622-522-1.rpt

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 12:04:55 ; Search time 23.08 Seconds

(without alignments)  
739.487 Million cell updates/sec

Title: US-09-622-522-1

Perfect score: 698  
Sequence: 1 MHFLFRFIVFFYLMGLFTFAQ.....PPSFAYGKRGYDKPLAKGI 129

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP unclassified: \*  
13: SP vertebrate: \*  
14: SP virus: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	653	93.6	259	4 Q9Y680	Q9Y680 homo sapien
2	648	92.8	222	4 Q9Y680	Q9Y680 homo sapien
3	553	79.2	218	11 O54998	O54998 mus musculu
4	271.5	38.9	211	4 Q9Y680	Q9Y680 homo sapien
5	223	31.9	216	5 Q9Y680	Q9Y680 homo sapien
6	220	31.5	216	5 Q9Y680	Q9Y680 homo sapien
7	206.5	29.6	137	5 Q9Y680	Q9Y680 homo sapien
8	205.5	29.4	139	5 Q9Y680	Q9Y680 homo sapien
9	204.5	29.3	261	5 Q9Y680	Q9Y680 homo sapien
10	196.5	28.2	138	5 Q9Y680	Q9Y680 homo sapien
11	193.5	27.7	137	5 Q9Y680	Q9Y680 homo sapien
12	193.5	27.7	137	5 Q9Y680	Q9Y680 homo sapien
13	190	27.2	481	4 Q9Y680	Q9Y680 homo sapien
14	189.5	27.1	137	5 Q9Y680	Q9Y680 homo sapien
15	187.5	26.9	517	4 Q9Y680	Q9Y680 homo sapien
16	187.5	26.9	570	11 Q9Y680	Q9Y680 homo sapien
17	187	26.8	582	4 Q9Y680	Q9Y680 homo sapien
18	186.5	26.7	163	10 Q9Y680	Q9Y680 homo sapien
19	186.5	26.7	163	10 Q9Y680	Q9Y680 homo sapien

20	180	25.8	151	10 Q41649	Q41649 vicia faba
21	179.5	25.7	570	11 Q9Y680	Q9Y680 mus musculu
22	178.5	25.6	146	10 Q38935	Q38935 arabidopsis
23	178.5	25.6	153	10 Q9L5F4	Q9L5F4 arabidopsis
24	178	25.4	134	5 Q17280	Q17280 botryllus s
25	177.5	25.4	577	13 Q9YIC3	Q9YIC3 gallus gall
26	175	25.1	262	4 Q9U6J3	Q9U6J3 homo sapien
27	175	25.1	355	4 Q9H6J3	Q9H6J3 homo sapien
28	172.5	24.7	264	5 Q9H1B0	Q9H1B0 caenorhabdi
29	166.5	23.9	164	5 Q908J8	Q908J8 brugia mala
30	163.5	23.4	201	4 Q9NYL4	Q9NYL4 homo sapien
31	162	23.2	119	13 Q9DFL8	Q9DFL8 gillithyris
32	158.5	22.7	259	5 Q23338	Q23338 caenorhabdi
33	157.5	22.6	578	10 Q9YFJ3	Q9YFJ3 arabidopsis
34	153.5	22.0	201	2 Q9YFJ3	Q9YFJ3 arabidopsis
35	145	20.8	152	2 Q9YFJ3	Q9YFJ3 arabidopsis
36	141	20.2	551	10 Q38931	Q38931 arabidopsis
37	141	20.2	551	10 Q38949	Q38949 arabidopsis
38	141	20.2	555	10 Q9L5F3	Q9L5F3 arabidopsis
39	137.5	19.7	108	5 Q9Y8S8	Q9Y8S8 drosophila
40	137.5	19.7	487	10 Q9STK2	Q9STK2 arabidopsis
41	137	19.6	143	10 Q9YFJ3	Q9YFJ3 arabidopsis
42	129.5	18.6	108	5 Q904Z3	Q904Z3 manduca sex
43	129.5	18.6	457	6 Q9XSH5	Q9XSH5 salmire bol
44	128.5	18.4	208	10 Q9SCY2	Q9SCY2 arabidopsis
45	128.5	18.4	349	5 Q9YF88	Q9YF88 drosophila

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	259 AA.
ID	Q9Y680			
AC	Q9Y680			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	FK506-BINDING PROTEIN FRB23 ISOFORM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PIUTARY TUMOR;			
RA	Guan Z., Zhang Q., Dai M., Song H., Mao Y., Wu X., Mao M., Fu G.,			
RA	Luo M., Chen J., Hu R.;			
RT	"Human FK506-binding Protein (FKBP23)-isoform gene."			
RL	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.			
CC	-I- SIMILARITY: TO EF-HAND FAMILY.			
DR	EMBL: AF100751; AAD43015.1; -			
DR	HSSP: P20081; IYAT.			
DR	InterPro: IPR000886; -			
DR	InterPro: IPR001179; -			
DR	InterPro: IPR002048; -			
DR	Pfam: PF00036; ehand; 2.			
DR	Pfam: PF00254; FKBP; 2.			
DR	PROSITE: PS00018; EF_HAND; UNKNOWN_2.			
DR	PROSITE: PS00014; EF_TARGET; UNKNOWN_1.			
DR	PROSITE: PS00454; FKBP_PPIASE_2; UNKNOWN_1.			
DR	PROSITE: PS00059; FKBP_PPIASE_3; 1.			
KW	Calcium-binding.			
SO	SEQUENCE 259 AA; 30009 MW; 886A1F3F5ACB9E78 CRC64;			
Query Match	93.6%; Score 653; DB 4; Length 259;			
Best local Similarity	100.0%; Pred. No. 3.1e-61;			
Matches 120; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 MHFLFRFIVFFYLMGLFTFAQROKKESTEVEKIEVLHHPENCSTSKKGLLNHYGYL 60			
DB	5 MHFLFRFIVFFYLMGLFTFAQROKKESTEVEKIEVLHHPENCSTSKKGLLNHYGYL 64			

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QY 61 AKDSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||
DB 65 AKDSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 124
|||||

RESULT 2
QY6B0 PRELIMINARY: PRT: 222 AA.
AC QY6B0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FK506-BINDING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-NORMAL PITUITARY;
RA Han Z., Song H., Dai M., Huang Q., Mao Y., Zhang Q., Mao M., Fu G.,
Luo M., Chen J., Hu R.;
RT "Human FK506-binding protein mRNA, complete cds.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AF092137; AAD40379.1; -.
DR HSSP; AF092137; AAD40379.1; -.
DR InterPro; IPR000886; -.
DR InterPro; IPR001179; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; ehand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Calcium-binding.
SQ SEQUENCE 222 AA; 25768 MW; 376C4CBB78DF730D CRC64;

Query Match 92.8%; Score 648; DB 4; Length 222;
Best local similarity 99.2%; Pred. No. 8,7e-61;
Matches 119; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHFLRFVFFYLMGLFTAQORKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 60
|||||
DB 5 MHFLRFVFFYLMGLFTAQORKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 64
|||||

QY 61 AKDSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||
DB 65 AKDSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 124
|||||

RESULT 3
QY6B0 PRELIMINARY: PRT: 218 AA.
AC QY6B0;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FK506-BINDING PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIH/SWISS;
RA Nakamura T., Yabe D., Kanazawa N., Tashiro K., Sasayama S., Honjo T.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: TO EF-HAND FAMILY.

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DR EMBL; AF040252; AAC79959.1; -.
DR HSSP; P20081; 1YAT
DR MGI; MGI:1336879; FKBP7.
DR InterPro; IPR000886; -.
DR InterPro; IPR001179; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding.
SQ SEQUENCE 218 AA; 24913 MW; DB0AE509E60EEBA CRC64;

Query Match 79.2%; Score 553; DB 11; Length 218;
Best local similarity 85.8%; Pred. No. 9.6e-51;
Matches 103; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 MHFLRFVFFYLMGLFTAQORKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 60
|||||
DB 1 MHFLRFVFFYLMGLFTAQORKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 60
|||||

QY 61 AKDSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||
DB 61 AKDSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 120
|||||

RESULT 4
QY6B0 PRELIMINARY: PRT: 211 AA.
AC QY6B0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CDNA FLJ20731 FIS, CLONE HEP10272.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Odayashi M.,
Nishi T., Shibahara T., Tanaka T., Nakamura Y., Iisaga T., Sugano S.;
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: TO EF-HAND FAMILY.
CC EMBL; AK000738; BAA91351.1; -.
DR EMBL; AK000738; BAA91351.1; -.
DR InterPro; IPR000886; -.
DR InterPro; IPR001179; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Calcium-binding.
SQ SEQUENCE 211 AA; 24172 MW; 858184954FE10029 CRC64;

Query Match 38.9%; Score 271.5; DB 4; Length 211;
Best local similarity 44.2%; Pred. No. 5.7e-21;
Matches 53; Conservative 20; Mismatches 42; Indels 5; Gaps 1;

QY 3 FLRFVFFYLMGLFTAQORKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 62
|||||
DB 4 FLRFVFFYLMGLFTAQORKEESTEEVYKIEVLHREPCSKTSKGGDLNAHYDYL 58
|||||

QY 63 DGSKFCYCSRTQNEGHPKMFVLGVGVKIGLDIAMTDMCPGKRRKVIIPSPFAYGKEGY 122
|||||

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Db 59 DGSIFHSHHNNQPIWFTLGLTLEALKMGDGLKMGCVGEKRLIIPALGYGKEGK 118

RESULT 5  
ID 09X254 PRELIMINARY; PRT: 216 AA.

AC 09X254: 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE BCDNA:GM07659.  
GN FKBP13 OR BCDNA:GM07659 OR BCDNA:GH08925 OR CG9847.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tsang S.E., Brokstein P., Frise E., Harvey D., Evans-Holm M.,  
RA Lewis S.E., Sun C., Rubin G.M.;  
RT "Full Length Drosophila melanogaster cDNA sequence."  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO EF-HAND FAMILY.  
DR EMBL: AF132555; AAD27854.1; -  
DR HSSP: P20081; 1YAT.  
DR Pibase: FBgn0010470; FKbp13.  
DR InterPro: IPR000886; -  
DR InterPro: IPR001179; -  
DR Pfam: IPR002048; -  
DR Pfam: PF00036; ehand; 2.  
DR Pfam: PF00254; FKBP; 1.  
DR PROSITE: PS00018; EF\_HAND; UNKNOWN\_2.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
DR PROSITE: PS50059; FKBP\_PPIASE\_3; 1.  
DR SMART: SM00054; Eph; 1.  
KW Calcium-binding.  
SQ SEQUENCE 216 AA; 23960 MW; E1AEAD276766C9C8 CRC64;

Query Match 31.9%; Score 223; DB 5; Length 216;  
Best Local Similarity 49.5%; Pred. No. 7.9e-16;  
Matches 45; Conservative 12; Mismatches 32; Indels 2; Gaps 1;

QY 29 EEKIVLHREPNCSTKSKGDLNHYGYLAKDSKRYCSTQNEGHPKMFVLGCV 88  
DB 24 EDKVEVISTPEVCEQSKNKGSLTMYHTGLQADGKFFDSFDRDQ--PFTFLGAGV 81  
QY 89 IKGLDAMTDMPGKRRKVVPPSFAYKRG 119  
DB 82 IKGMDOGILMCMYGEKRRKLTIPOLGYGDOG 112

RESULT 6  
ID 09V3V2 PRELIMINARY; PRT: 216 AA.

AC 09V3V2: 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE FKBP13 PROTEIN.  
GN FKBP13 OR BCDNA:GM07659 OR BCDNA:GH08925 OR CG9847.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-BERKELEY;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Genter A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doop L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merulov G., Mishina N.V., Modarity C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klimos I., Simpson M., Skipski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,  
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,  
RA Agbayani A., Arcaina T.T., Baxter E., Blazer R.G., Butenhoff C.,  
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.B., Frise E.,  
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,  
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,  
RA Park S., Sequeira A., Sethi H., Snir E., Svitskas R.R., Weinburg T.,  
RA Celniker S.E.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO EF-HAND FAMILY.  
DR EMBL: AE003454; AAF46726.1; -  
DR EMBL: AF132154; AAD34742.1; -  
DR HSSP: P20081; 1YAT.  
DR Pibase: FBgn0010470; FKbp13.  
DR InterPro: IPR000886; -  
DR InterPro: IPR001179; -  
DR InterPro: IPR002048; -  
DR Pfam: PF00036; ehand; 2.  
DR Pfam: PF00254; FKBP; 1.  
DR PROSITE: PS00018; EF\_HAND; 2.  
DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE: PS00454; FKBP\_PPIASE\_2; 1.  
DR PROSITE: PS50059; FKBP\_PPIASE\_3; 1.  
DR SMART: SM00054; Eph; 1.  
KW Calcium-binding; Hypothetical protein.  
SQ SEQUENCE 216 AA; 23960 MW; 5A8501C02DDA2E80 CRC64;

Query Match 31.5%; Score 220; DB 5; Length 216;  
Best Local Similarity 48.4%; Pred. No. 1.6e-15;  
Matches 44; Conservative 13; Mismatches 32; Indels 2; Gaps 1;

QY 29 EEKIVLHREPNCSTKSKGDLNHYGYLAKDSKRYCSTQNEGHPKMFVLGCV 88  
DB 24 EDKVEVISTPEVCEQSKNKGSLTMYHTGLQADGKFFDSFDRDQ--PFTFLGAGV 81

QY 89 IKGIDIAMTDMCPGKRRKVVIPSPFAYGKEG 119  
 DB 82 IKGMDGILNMCYGEKRLITPPLGVDG 112

RESULT 7  
 ID 096335 PRELIMINARY; PRT; 137 AA.  
 AC 096335;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE PPTIDYL-PROLYL CIS-TRANS ISOMERASE.  
 GN FKBP13.  
 OS Brugia malayi.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Brugia.  
 OC NCBI\_Taxid=6279;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT Ma D., Hong X.Q., Carlow C.K.S.;  
 "A FK506-insensitive small molecular weight FKBP of filarial  
 parasites."  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016454; AAD01595.1; -  
 DR HSSP; P20071; 1FKJ.  
 DR InterPro; IPR001179; -  
 DR Pfam; PF00254; FKBP; 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
 DR Isomerase.  
 KW SEQUENCE 137 AA; 15270 MW; 0F3E0C363768D91E CRC64;  
 SQ

Query Match 29.6%; Score 206.5; DB 5; Length 137;  
 Best Local Similarity 45.3%; Pred. No. 2.5e-14;  
 Matches 43; Conservative 18; Mismatches 31; Indels 3; Gaps 2;

QY 25 EESTEEVKIEVLHPENCSTKSKGDDLNAHYDGLAKDGSKEFCSTQNEGHPKFWLG 84  
 DB 20 DKEARLQIGYKRRVDCNERSKGDILNHYVGM-EDGTEFDSRRNK--PFTTLG 76  
 QY 85 VGOVIKGIAMTDMCPGKRRKVVIPSPFAYGKEG 119  
 DB 77 MGOVIKGMDOGLNMCYGEKRLITPPLGVDG 111

RESULT 8  
 ID 020107 PRELIMINARY; PRT; 139 AA.  
 AC 020107;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE F36H1.1 PROTEIN.  
 GN F36H1.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT Kershaw J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
 Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 Gardner A., Green P., Hawkins J., Kirsten J., Laister N., Latreille P.,  
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,  
 Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,  
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans."  
 RT Nature 368:32-38(1994).  
 RL EMBL; Z68760; CA92994.1; -  
 DR HSSP; P18203; 1ERL.  
 DR InterPro; IPR001179; -  
 DR Pfam; PF00254; FKBP; 1.  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1; 1.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; 1.  
 DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
 SQ SEQUENCE 139 AA; 15472 MW; A1AE973B1D0ED5F6 CRC64;

Query Match 29.4%; Score 205.5; DB 5; Length 139;  
 Best Local Similarity 46.3%; Pred. No. 3.3e-14;  
 Matches 44; Conservative 16; Mismatches 32; Indels 3; Gaps 2;

QY 25 EESTEEVKIEVLHPENCSTKSKGDDLNAHYDGLAKDGSKEFCSTQNEGHPKFWLG 84  
 DB 21 EOKIDKIQIGYKRRVDCNERSKGDILNHYVGM-EDGTEFDSRRNK--PFTTLG 77  
 QY 85 VGOVIKGIAMTDMCPGKRRKVVIPSPFAYGKEG 119  
 DB 78 QGVIKGMDOGLNMCYGEKRLITPPLGVDG 112

RESULT 9  
 ID 016309 PRELIMINARY; PRT; 261 AA.  
 AC 016309;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE C05C8.3 PROTEIN.  
 GN C05C8.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
 Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 Gardner A., Green P., Hawkins J., Kirsten J., Laister N., Latreille P.,  
 Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 Parsons J., Percy C., Rifken L., Roopra A., Mortimore B., O'Callaghan M.,  
 Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,  
 "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans."  
 RT Nature 368:32-38(1994).  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Sammons L., Wohlmann P.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016430; AAB65370.1; -  
 DR HSSP; P27124; 1ROT.



## RESULT 12

ID Q918P8 PRELIMINARY; PRT; 564 AA.

AC Q918P8; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE FK506-BINDING PROTEIN.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20302564; PubMed=10842073;

RA Spokony R., Saint-Jeanne J.-P.,

RT "Xenopus FK 506-binding protein, a novel immunophilin expressed during

RT early development."

RL Mech. Dev. 94:205-208(2000).

CC -1- SIMILARITY: TO EF-HAND FAMILY.

DR EMBL: AF332672; AAF5906.1; -

DR InterPro: IPR001179; -

DR InterPro: IPR002048; -

DR Pfam: PF00254; eHand; 2.

DR PROSITE: PS00018; EF\_HAND; UNKNOWN\_1.

DR PROSITE: PS00014; ER\_TARGET; UNKNOWN\_1.

DR PROSITE: PS00054; FKBP\_PPIASE\_3; 4.

DR SMART: SM00054; EFN; 1.

DR Calcium-binding.

SQ SEQUENCE 564 AA; 62643 MW; 15312365BF1E43CF CRC64;

Query Match 27.7%; Score 193.5; DB 13; Length 564;

Best Local Similarity 38.6%; Pred. No. 3.3e-12; Matches 39; Conservative 22; Mismatches 31; Indels 9; Gaps 3;

QY 29 EEVIEVLRHRENCSTKSKGDLNAHYDGLARKSGKFCSTQNGHPRKFWLVGVGV 88

DB 361 DSVIEVHKKRDCSTNTSKGDFIKYHNCML-DGTLFSSHEYE--PQVVLGSSSK 417

QY 89 IKGLDIAMTDMCPGKKRVVIPPSEFAYGKEGYDKPLAKGI 129

DB 418 IEGDLTGILGMCYGERRTVLVPHLHGSG-----ARGV 452

RESULT 13

ID Q9H6N5 PRELIMINARY; PRT; 481 AA.

AC Q9H6N5; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE CDNA: FLJ22041 FIS, CLONE HEP9061.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,

RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,

RT "NEO human cDNA sequencing project."

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AK025694; BAB15220.1; -

SQ SEQUENCE 481 AA; 53219 MW; AAD5181BFC88BDFE CRC64;

Query Match 27.2%; Score 190; DB 4; Length 481;

Best Local Similarity 35.0%; Pred. No. 6.4e-12; Matches 41; Conservative 26; Mismatches 36; Indels 14; Gaps 4;

QY 4 LRFVIEVLRHRENCSTKSKGDLNAHYDGLARKSGKFCSTQNGHPRKFWLVGVGV 63

DB 39 LYEDVLLDW-----NKEDT---VQSTLLRPPHCPRMVODGDFRVHYNGTLL-D 86

QY 64 GSKFYCSRTQNGHPRKFWLVGVGVYKGLDIAMTDMCPGKKRVVIPPSEFAYGKEG 120

DB 87 GTSFDTYSKSGGVYDTY--VSGWLIKGMDOGLGMCPEKRRKIIIPFLAYGEGY 141

RESULT 14

ID Q96336 PRELIMINARY; PRT; 137 AA.

AC Q96336; 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.

GN FKBP13.

OS Onchocerca volvulus.

OC Eukaryota; Metazoa; Nematoda; Spirurida; Filarioidea;

OC Onchocercidae; Onchocerca.

OX NCBI\_TaxID=6282;

RN [1]

RP SEQUENCE FROM N.A.

RA "A D., Hong X.Q., Carlow C.K.S.,

RT "A FK506-insensitive small molecular weight FKBP of filarial

RT parasites."

RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF016455; AAD01596.1; -

DR HSSP: P20071; 1PKJ.

DR InterPro: IPR001179; -

DR Pfam: PF00254; FKBP\_PPIASE\_2; 1.

DR PROSITE: PS00054; FKBP\_PPIASE\_3; 1.

DR PROSITE: PS00059; FKBP\_PPIASE\_3; 1.

DR Isomerase.

SQ SEQUENCE 137 AA; 15408 MW; 13CE5F7E5ABAEED38 CRC64;

Query Match 27.1%; Score 189.5; DB 5; Length 137;

Best Local Similarity 44.9%; Pred. No. 1.6e-12; Matches 40; Conservative 18; Mismatches 28; Indels 3; Gaps 2;

QY 31 VKTEVLRHRENCSTKSKGDLNAHYDGLARKSGKFCSTQNGHPRKFWLVGVGVYK 90

DB 26 LQIGVKKRDNCEIRSKGDIVVHYVGM-EDGTEFDNIRFRNK--PIFTLGMGVYK 82

QY 91 GLDIAMTDMCPGKKRVVIPPSEFAYGKEG 119

DB 83 GWDGILLNMGEGRRLLALPSDLAYGSGF 111

RESULT 15

ID Q95302 PRELIMINARY; PRT; 517 AA.

AC Q95302; 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE FK506-BINDING PROTEIN (FRAGMENT).

GN FKBP63.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Shaddy M., Caubit X., Krauss S.,

RT "Human FK506 binding protein, homolog to mouse FKBP63."

RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO EF-HAND FAMILY.  
DR EMBL; AF089745; AAC78853.1; -.  
DR HSSP; P20081; 1YAT.  
DR InterPro; IPR000886; -.  
DR InterPro; IPR001179; -.  
DR InterPro; IPR002048; -.  
DR Pfam; PF00036; efhand; 2.  
DR Pfam; PF00234; FKBP; 4.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN\_1.  
DR PROSITE; PS00454; FKBP\_PPIASE\_2; UNKNOWN\_3.  
DR PROSITE; PS50059; FKBP\_PPIASE\_3; 4.  
DR SMART; SM00054; EFh; 1.  
KW Calcium-binding.  
FT NON\_TER 1  
SQ SEQUENCE 517 AA; 57219 MW; 704FB0CE9C44C74B CRC64;

Query Match 26.98; Score 187.5; DB 4; Length 517;  
Best Local Similarity 42.68; Pred. No. 1.3e-11;  
Matches 40; Conservative 15; Mismatches 36; Indels 3; Gaps 2;

QY 28 TEEVKIEVLHREPENCSTKSKGDLNAHYDGLAKDSKFCSTRTONEGHIPKMFVLGVGQ 87  
DB 315 SDSISITSHKPPDCSVLSKKGDYLYKHYNASL-DGT--LDSFWNLGKTYNIVLGSQ 371  
QY 88 VIRGLDIAMTDMCPGCKKRVVIPPFAVYKGEYD 121  
DB 372 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAYD 405

Search completed: August 31, 2001, 12:06:41  
Job time: 106 sec

